

STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 96021

To: Mary Schmidt
Location: CM1-11E12
Art Unit: 1635
Monday, June 16, 2003

Case Serial Number: 09/532001

From: Beverly Shears
Location: Biotech-Chem Library
CM1-1E05
Phone: 308-4994

beverly.shears@uspto.gov

Search Notes

)

STIC-Biotech/ChemLib

96021

From: Hutzell, Paula
Sent: Friday, June 06, 2003 12:01 PM
To: Schmidt, Mary; STIC-Biotech/ChemLib; Chan, Christina
Subject: RE: RUSH sequence search request 09/532,001

approved

-----Original Message-----

Fr m: Schmidt, Mary
Sent: Friday, June 06, 2003 11:59 AM
To: Hutzell, Paula
Subject: FW: RUSH sequence search request 09/532,001

CRF

Hi, according to Christine's out of office message, we should send rush requests to you...

-----Original Message-----

Fr m: Schmidt, Mary
Sent: Friday, June 06, 2003 11:57 AM
T : Chan, Christina
Subject: FW: RUSH sequence search request 09/532,001

Hi, do you submit sequence search requests? Jeff and Jim are out of the office. If not, could you let me know who else does?

thanks,
Melissa

-----Original Message-----

Fr m: Schmidt, Mary
Sent: Friday, June 06, 2003 11:56 AM
T : Martinell, James
Subject: FW: RUSH sequence search request 09/532,001

Hi, Jeff is out today, if you are in, could you submit?
thanks,
Melissa

-----Original Message-----

Fr m: Schmidt, Mary
Sent: Friday, June 06, 2003 11:55 AM
To: Fredman, Jeffrey
Subject: RUSH sequence search request 09/532,001

I missed a sequence in the claims and this is a two month amended.

Please search SEQ ID NO:1 in nucleic acid databases. Please search both SEQ ID NO:1 as well as the complement sequence. Please size limit the results to less than 50 bases (so that in the results only hits less than 50 bases will appear).

Thanks,
Melissa Schmidt
11d05
mailboxes 11e12

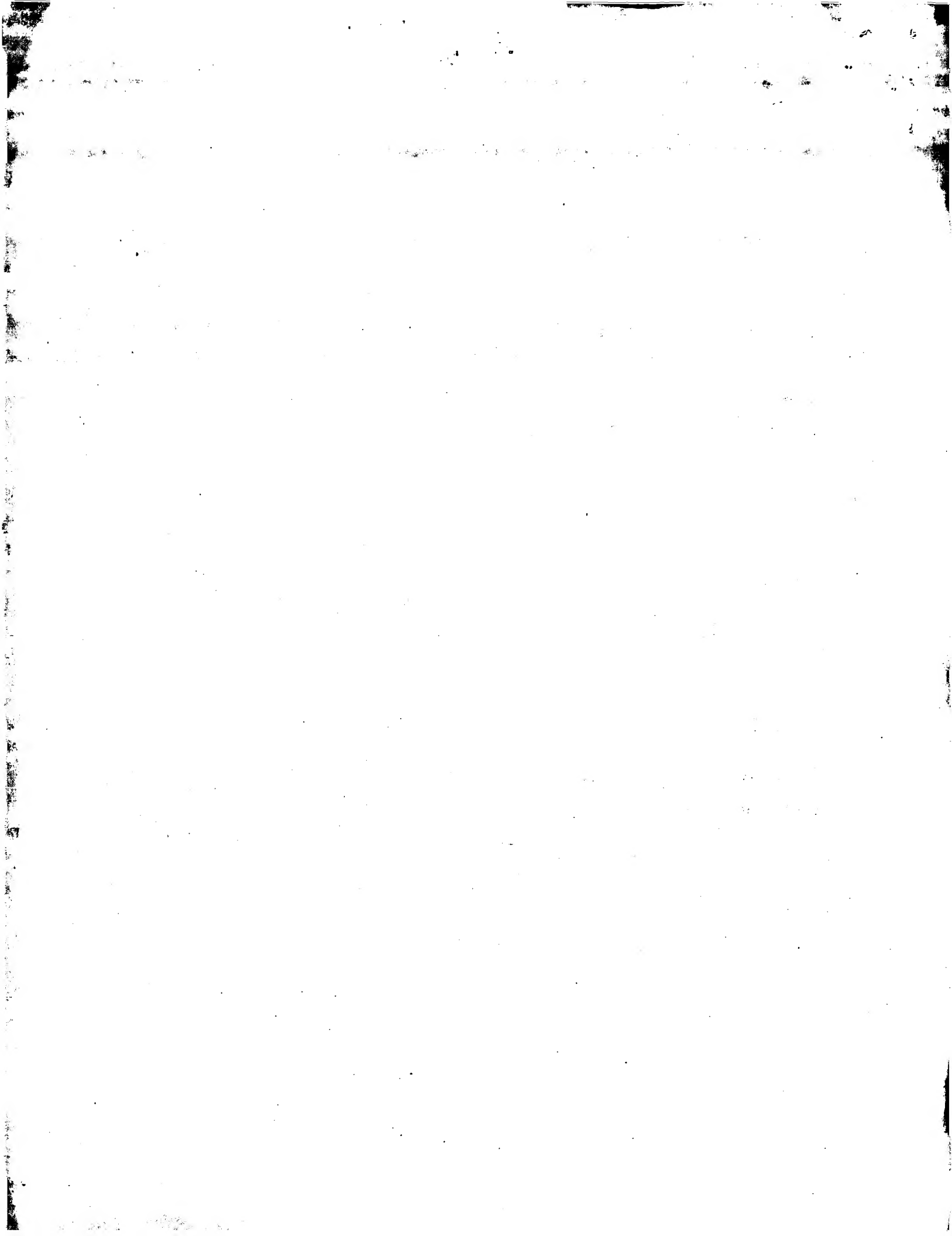
Searcher: _____
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: _____
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:

NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)

STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____



au 1635
308-4471

96.021

Searcher: _____
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TYPE OF SEARCH:

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AA Sequences: _____
Structures: _____
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Patent Family: _____
Other: _____

VENDOR/COST (where applic.)

STN: _____
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Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

SEARCH REQUEST FORM

Requestor's Name: _____ Serial Number: _____

Date: _____ Phone: _____ Art Unit: _____

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

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STAFF USE ONLY

Date completed: 06-16-03

Searcher: Beverly C4994

Terminal time: 21

Elapsed time: _____

CPU time: _____

Total time: 24

Number of Searches: _____

Number of Databases: 1

Search Site

_____ STIC

_____ CM-1

_____ Pre-S

Type of Search

_____ N.A. Sequence

_____ A.A. Sequence

_____ Structure

_____ Bibliographic

Vendors

_____ IG

☒ STN

_____ Dialog

_____ APS

_____ Geninfo

_____ SDC

_____ DARC/Questel

☒ Other CGN

09/532001

FILE 'REGISTRY' ENTERED AT 09:51:15 ON 16 JUN 2003
L1 1 S CTGAGACCGATATCGGTCTCAG/SQSN
L1 ANSWER 1 OF 1 REGISTRY COPYRIGHT 2003 ACS
RN 214357-65-0 REGISTRY
CN DNA, d(C-T-G-A-G-A-C-C-G-A-T-A-T-C-G-G-T-C-T-C-A-G) (9CI) (CA INDEX
NAME)
CI MAN
SQL 22

SEQ 1 ctgagaccga tatcgggtctc ag
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HITS AT: 1-22

REFERENCE 1: 129:301741

FILE 'HCAPLUS' ENTERED AT 09:52:34 ON 16 JUN 2003
L2 1 S L1

L2 ANSWER 1 OF 1 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1998:682556 HCAPLUS
DOCUMENT NUMBER: 129:301741
TITLE: Production of functional proteins: balance of
shear stress and gravity
INVENTOR(S): Goodwin, Thomas John; Hammond, Timothy Grant;
Kaysen, James Howard
PATENT ASSIGNEE(S): The United States of America as Represented by
the Administrator of the National Aeronautics
and Space Administration, USA; Administrators of
the Tulane Education Fund
SOURCE: PCT Int. Appl., 56 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9845468	A1	19981015	WO 1998-US6826	19980407
W:	AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG			
AU 9869534	A1	19981030	AU 1998-69534	19980407
EP 972069	A1	20000119	EP 1998-915320	19980407
R:	AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI			
BR 9808510	A	20000523	BR 1998-8510	19980407
JP 2001517081	T2	20011002	JP 1998-540983	19980407
PRIORITY APPLN. INFO.:			US 1997-43205P	P 19970408
			WO 1998-US6826	W 19980407
AB	The present invention provides a method for prodn. of functional			

09/532001

proteins, including hormones, by renal cells in a 3-dimensional co-culture process responsive to shear stress using a rotating wall vessel. Natural mixt. of renal cells expresses the enzyme 1.alpha.-hydroxylase, which can be used to generate the active form of vitamin D - 1,25-diOH vitamin D3. The fibroblast cultures and co-culture of renal cortical cells express the gene for erythropoietin and secrete erythropoietin into the culture supernatant. Other shear stress response genes are also modulated by shear stress, such as toxin receptors megalin and cubulin (gp280). Also provided is a method of treating in-need individual with the functional proteins produced in a 3-dimensional co-culture process responsive to shear stress using a rotating wall vessel.

IT 214357-65-0

RL: BUU (Biological use, unclassified); BIOL (Biological study);

USES (Uses)

(prodn. of functional proteins: balance of shear stress and gravity)

REFERENCE COUNT:

7

THERE ARE 7 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

FILE 'HOME' ENTERED AT 09:52:44 ON 16 JUN 2003

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 14, 2003, 21:58:21 ; Search time 2130 Seconds
(without alignments)
259.688 Million cell updates/sec

Title: US-09-532-001-1

Perfect score: 22
Sequence: 1 CTGAGACCGATATCGTCTCAG 22

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters: 12114646

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 26	14.2	64.5	25	79	US-60-353-987-90477	Sequence 90477, A	C 99	13.6	61.8	25	36	US-60-233-166-41182	Sequence 41182,
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C 35	14.2	64.5	28	17	US-09-310-735C-30	Sequence 30, App1	C 108	13.6	61.8	25	79	US-60-353-987-700753	Sequence 700753,
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C 38	14.2	64.5	28	17	US-09-310-762-30	Sequence 30, App1	C 111	13.6	61.8	31	18	US-09-665-684-164	Sequence 164, App
C 39	14.2	64.5	28	17	US-09-310-762A-30	Sequence 30, App1	C 112	13.4	60.9	25	36	US-09-954-427-261696	Sequence 261696,
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C 69	14	63.6	25	79	US-60-353-987-802554	Sequence 802554,	C 142	13.2	60.0	25	36	US-09-954-427-385675	Sequence 385675,
C 70	14	63.6	40	17	US-09-324-672A-111	Sequence 111, App	C 143	13.2	60.0	25	36	US-09-954-427-385675	Sequence 385675,
C 71	13.8	62.7	25	36	US-09-954-427-32867	Sequence 32867, A	C 144	13.2	60.0	25	36	US-09-956-584-223371	Sequence 223371,
C 72	13.8	62.7	25	36	US-09-954-427-32867	Sequence 32867, A	C 145	13.2	60.0	25	36	US-09-956-584-382522	Sequence 382522,
C 73	13.8	62.7	25	36	US-09-954-427-32867	Sequence 32867, A	C 146	13.2	60.0	25	36	US-09-956-584-382522	Sequence 382522,
C 74	13.8	62.7	25	36	US-09-954-427-32867	Sequence 32867, A	C 147	13.2	60.0	25	36	US-09-956-584-481273	Sequence 481273,
C 75	13.8	62.7	25	36	US-09-956-584-2696	Sequence 2696, Ap	C 148	13.2	60.0	25	36	US-09-956-584-481273	Sequence 481273,
C 76	13.8	62.7	25	36	US-09-956-584-2696	Sequence 2696, Ap	C 149	13.2	60.0	25	36	US-09-956-604-132887	Sequence 132887,
C 77	13.8	62.7	25	36	US-09-956-584-2711	Sequence 2711, Ap	C 150	13.2	60.0	25	36	US-09-956-604-132887	Sequence 132887,
C 78	13.8	62.7	25	36	US-09-956-584-2711	Sequence 2711, Ap	C 151	13.2	60.0	25	36	US-09-956-604-132887	Sequence 132887,
C 79	13.8	62.7	25	36	US-09-956-584-53197	Sequence 53197, A	C 152	13.2	60.0	25	36	US-09-956-604-132887	Sequence 132887,
C 80	13.8	62.7	25	36	US-09-956-584-53197	Sequence 53197, A	C 153	13.2	60.0	25	36	US-09-956-604-132887	Sequence 132887,
C 81	13.8	62.7	25	67	US-60-233-166-32867	Sequence 32867, A	C 154	13.2	60.0	25	36	US-09-956-604-132887	Sequence 132887,
C 82	13.8	62.7	25	67	US-60-233-166-32867	Sequence 32867, A	C 155	13.2	60.0	25	67	US-60-232-638-90122	Sequence 90122, A
C 83	13.8	62.7	25	67	US-60-233-166-32867	Sequence 32867, A	C 156	13.2	60.0	25	67	US-60-232-638-90122	Sequence 90122, A
C 84	13.8	62.7	25	67	US-60-233-166-32867	Sequence 32867, A	C 157	13.2	60.0	25	67	US-60-233-166-34972	Sequence 34972, A
C 85	13.8	62.7	25	67	US-60-233-166-32867	Sequence 32867, A	C 158	13.2	60.0	25	67	US-60-233-166-34972	Sequence 34972, A
C 86	13.8	62.7	25	67	US-60-234-017-16155	Sequence 16155, A	C 159	13.2	60.0	25	67	US-60-233-166-43710	Sequence 43710, A
C 87	13.8	62.7	25	67	US-60-234-017-16155	Sequence 16155, A	C 160	13.2	60.0	25	67	US-60-233-166-43710	Sequence 43710, A
C 88	13.8	62.7	25	67	US-60-234-017-1978	Sequence 31978, A	C 161	13.2	60.0	25	67	US-60-233-166-88029	Sequence 88029, A
C 89	13.8	62.7	25	67	US-60-234-017-1978	Sequence 31978, A	C 162	13.2	60.0	25	67	US-60-233-166-88029	Sequence 88029, A
C 90	13.8	62.7	25	67	US-60-234-017-1990	Sequence 31990, A	C 163	13.2	60.0	25	67	US-60-233-166-121920	Sequence 121920,
C 91	13.8	62.7	25	67	US-60-234-017-1990	Sequence 31990, A	C 164	13.2	60.0	25	67	US-60-233-166-121920	Sequence 121920,
C 92	13.8	62.7	25	79	US-60-353-987-320105	Sequence 320105,	C 165	13.2	60.0	25	67	US-60-353-987-320105	Sequence 159861,
C 93	13.8	62.7	25	79	US-60-353-987-320105	Sequence 320105,	C 166	13.2	60.0	25	67	US-60-353-987-320105	Sequence 159861,
C 94	13.8	62.7	25	79	US-60-353-987-559692	Sequence 559692,	C 167	13.2	60.0	25	67	US-60-353-987-559692	Sequence 253045,

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C 169	13.2	60.0	25	67	US-60-233-166-385675	Sequence 385675,	C 242	13	59.1	25	67	US-60-234-017-1756	Sequence 1756, Ap
C 170	13.2	60.0	25	67	US-60-233-166-385675	Sequence 385675,	C 243	13	59.1	25	67	US-60-234-017-155659	Sequence 155659,
C 171	13.2	60.0	25	67	US-60-234-017-219112	Sequence 219112,	C 244	13	59.1	25	67	US-60-234-017-155659	Sequence 155659,
C 172	13.2	60.0	25	67	US-60-234-017-219112	Sequence 219112,	C 245	13	59.1	25	67	US-60-234-017-343129	Sequence 343129,
C 173	13.2	60.0	25	67	US-60-234-017-325329	Sequence 325329,	C 246	13	59.1	25	67	US-60-234-017-343129	Sequence 343129,
C 174	13.2	60.0	25	67	US-60-234-017-325329	Sequence 325329,	C 247	13	59.1	25	67	US-60-234-017-495976	Sequence 495976,
C 175	13.2	60.0	25	67	US-60-234-017-488667	Sequence 488667,	C 248	13	59.1	25	67	US-60-234-017-495976	Sequence 495976,
C 176	13.2	60.0	25	67	US-60-234-017-488667	Sequence 488667,	C 249	13	59.1	25	67	US-60-234-017-495976	Sequence 495976,
C 177	13.2	60.0	25	67	US-60-234-049-136309	Sequence 136309,	C 250	13	59.1	25	67	US-60-235-987-305911	Sequence 305911,
C 178	13.2	60.0	25	67	US-60-234-049-136309	Sequence 136309,	C 251	13	59.1	25	67	US-60-235-987-305911	Sequence 305911,
C 179	13.2	60.0	25	79	US-60-353-987-31235	Sequence 31235, A	C 252	13	59.1	25	79	US-60-353-987-371036	Sequence 371036,
C 180	13.2	60.0	25	79	US-60-353-987-31235	Sequence 31235, A	C 253	13	59.1	25	79	US-60-353-987-371036	Sequence 371036,
C 181	13.2	60.0	25	79	US-60-353-987-175333	Sequence 175333,	C 254	13	59.1	25	79	US-60-353-987-403225	Sequence 403225,
C 182	13.2	60.0	25	79	US-60-353-987-175333	Sequence 175333,	C 255	13	59.1	25	79	US-60-353-987-403225	Sequence 403225,
C 183	13.2	60.0	25	79	US-60-353-987-175334	Sequence 175334,	C 256	13	59.1	25	79	US-60-353-987-519794	Sequence 519794,
C 184	13.2	60.0	25	79	US-60-353-987-175334	Sequence 175334,	C 257	13	59.1	25	79	US-60-353-987-519794	Sequence 519794,
C 185	13.2	60.0	25	79	US-60-353-987-403952	Sequence 403952,	C 258	13	59.1	25	79	US-60-353-987-631872	Sequence 631872,
C 186	13.2	60.0	25	79	US-60-353-987-403952	Sequence 403952,	C 259	13	59.1	25	79	US-60-353-987-631872	Sequence 631872,
C 187	13.2	60.0	25	79	US-60-353-987-403952	Sequence 403952,	C 260	13	59.1	25	79	US-60-353-987-797529	Sequence 797529,
C 188	13.2	60.0	25	79	US-60-353-987-417966	Sequence 417966,	C 261	13	59.1	25	79	US-60-353-987-797529	Sequence 797529,
C 189	13.2	60.0	25	79	US-60-353-987-453403	Sequence 453403,	C 262	13	59.1	25	79	US-60-353-987-875225	Sequence 875225,
C 190	13.2	60.0	25	79	US-60-353-987-453403	Sequence 453403,	C 263	13	59.1	25	79	US-60-353-987-875225	Sequence 875225,
C 191	13.2	60.0	25	79	US-60-353-987-697333	Sequence 697333,	C 264	13	59.1	25	79	US-60-353-987-875225	Sequence 875225,
C 192	13.2	60.0	25	79	US-60-353-987-697333	Sequence 697333,	C 265	13	59.1	25	79	US-60-353-987-875225	Sequence 875225,
C 193	13.2	60.0	25	79	US-60-353-987-701360	Sequence 701360,	C 266	13	59.1	25	79	US-60-353-987-875225	Sequence 875225,
C 194	13.2	60.0	25	79	US-60-353-987-701360	Sequence 701360,	C 267	13	59.1	25	79	US-60-353-987-875225	Sequence 875225,
C 195	13.2	60.0	30	1	PCT-US02-25842-9130	Sequence 9130, Ap	C 268	13	59.1	33	38	US-10-011-931-56	Sequence 56, Appl
C 196	13.2	60.0	30	1	PCT-US02-25842-9130	Sequence 9130, Ap	C 269	13	59.1	33	38	US-10-011-931-56	Sequence 56, Appl
C 197	13.2	60.0	30	42	US-10-227-567-9130	Sequence 9130, Ap	C 270	13	59.1	33	38	US-10-011-931-57	Sequence 57, Appl
C 198	13.2	60.0	30	42	US-10-227-567-9130	Sequence 9130, Ap	C 271	13	59.1	33	38	US-10-011-931-57	Sequence 57, Appl
C 199	13	59.1	25	17	US-09-396-196F-53220	Sequence 53220, A	C 272	13	59.1	36	18	US-09-403-752A-49	Sequence 49, Appl
C 200	13	59.1	25	17	US-09-396-196F-53220	Sequence 53220, A	C 273	13	59.1	36	18	US-09-403-752A-49	Sequence 49, Appl
C 201	13	59.1	25	17	US-09-396-196F-53220	Sequence 53220, A	C 274	13	59.1	36	22	US-09-551-151-49	Sequence 49, Appl
C 202	13	59.1	25	17	US-09-396-196F-53220	Sequence 53220, A	C 275	13	59.1	36	22	US-09-551-151-49	Sequence 49, Appl
C 203	13	59.1	25	26	US-09-660-080-20407	Sequence 20407, A	C 276	13	59.1	44	11	US-08-728-463B-241	Sequence 241, App
C 204	13	59.1	25	26	US-09-660-080-20407	Sequence 20407, A	C 277	13	59.1	44	11	US-08-728-463B-241	Sequence 241, App
C 205	13	59.1	25	26	US-09-660-080-20408	Sequence 20408, A	C 278	13	59.1	44	11	US-08-728-463B-241	Sequence 241, App
C 206	13	59.1	25	26	US-09-660-080-20408	Sequence 20408, A	C 279	13	59.1	44	29	US-09-724-965-241	Sequence 241, App
C 207	13	59.1	25	26	US-09-660-220-15527	Sequence 15527, A	C 280	13	59.1	44	29	US-09-724-965-241	Sequence 241, App
C 208	13	59.1	25	26	US-09-660-220-15527	Sequence 15527, A	C 281	12.8	58.2	24	1	PCT-US99-08522-45	Sequence 45, Appl
C 209	13	59.1	25	36	US-09-954-427-167194	Sequence 167194, A	C 282	12.8	58.2	24	1	PCT-US99-08522-45	Sequence 45, Appl
C 210	13	59.1	25	36	US-09-954-427-167194	Sequence 167194, A	C 283	12.8	58.2	24	14	US-09-062-580-45	Sequence 45, Appl
C 211	13	59.1	25	36	US-09-954-427-321446	Sequence 321446, A	C 284	12.8	58.2	24	14	US-09-062-580-45	Sequence 45, Appl
C 212	13	59.1	25	36	US-09-954-427-321446	Sequence 321446, A	C 285	12.8	58.2	24	14	US-09-074-984-45	Sequence 45, Appl
C 213	13	59.1	25	36	US-09-954-427-321446	Sequence 321446, A	C 286	12.8	58.2	24	14	US-09-074-984-45	Sequence 45, Appl
C 214	13	59.1	25	36	US-09-954-427-370117	Sequence 370117, A	C 287	12.8	58.2	24	14	US-09-084-303A-45	Sequence 45, Appl
C 215	13	59.1	25	36	US-09-954-429A-10938	Sequence 10938, A	C 288	12.8	58.2	24	14	US-09-084-303A-45	Sequence 45, Appl
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C 219	13	59.1	25	36	US-09-956-584-165448	Sequence 165448, A	C 292	12.8	58.2	25	26	US-09-660-080-14713	Sequence 14713, A
C 220	13	59.1	25	36	US-09-956-584-165448	Sequence 165448, A	C 293	12.8	58.2	25	26	US-09-660-080-14714	Sequence 14714, A
C 221	13	59.1	25	36	US-09-956-584-373745	Sequence 373745, A	C 294	12.8	58.2	25	26	US-09-660-080-14714	Sequence 14714, A
C 222	13	59.1	25	36	US-09-956-584-373745	Sequence 373745, A	C 295	12.8	58.2	25	26	US-09-660-220-93360	Sequence 93360, A
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C 224	13	59.1	25	36	US-09-956-584-474573	Sequence 474573, A	C 297	12.8	58.2	25	36	US-09-953-115-15552	Sequence 15552, A
C 225	13	59.1	25	67	US-60-232-638-100771	Sequence 100771, A	C 298	12.8	58.2	25	36	US-09-953-115-15552	Sequence 15552, A
C 226	13	59.1	25	67	US-60-232-638-100771	Sequence 100771, A	C 299	12.8	58.2	25	36	US-09-954-427-29935	Sequence 29935, A
C 227	13	59.1	25	67	US-60-232-638-103668	Sequence 103668, A	C 300	12.8	58.2	25	36	US-09-954-427-29935	Sequence 29935, A
C 228	13	59.1	25	67	US-60-232-638-103668	Sequence 103668, A	C 301	12.8	58.2	25	36	US-09-954-427-321612	Sequence 321612, A
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C 232	13	59.1	25	67	US-60-233-166-321446	Sequence 321446, A	C 305	12.8	58.2	25	36	US-09-954-427-372328	Sequence 372328, A
C 233	13	59.1	25	67	US-60-233-166-370117	Sequence 370117, A	C 306	12.8	58.2	25	36	US-09-954-427-372328	Sequence 372328, A
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C 235	13	59.1	25	67	US-60-233-357-20249	Sequence 20249, A	C 308	12.8	58.2	25	36	US-09-954-427-414094	Sequence 414094, A
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C 237	13	59.1	25	67	US-60-233-620-21632	Sequence 21632, A	C 310	12.8	58.2	25	36	US-09-956-584-60546	Sequence 60546, A
C 238	13	59.1	25	67	US-60-233-620-21632	Sequence 21632, A	C 311	12.8	58.2	25	36	US-09-956-584-60547	Sequence 60547, A
C 239	13	59.1	25	67	US-60-233-620-68650	Sequence 68650, A	C 312	12.8	58.2	25	36	US-09-956-584-60547	Sequence 60547, A
C 240	13	59.1	25	67	US-60-233-620-68650	Sequence 68650, A	C 313	12.8	58.2	25	36	US-09-956-584-93765	Sequence 93765, A

C 314	12.8	58.2	25	36	US-09-956-584-93765	Sequence 93765, A	387	12.8	58.2	43	30	US-09-786-254-3	Sequence 3, Appli
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C 316	12.8	58.2	25	36	US-09-956-584-93773	Sequence 93773, A	C 389	12.8	58.2	43	30	US-09-786-254-4	Sequence 4, Appli
C 317	12.8	58.2	25	36	US-09-956-584-231127	Sequence 231127, A	C 390	12.8	58.2	43	30	US-09-786-254-4	Sequence 4, Appli
C 318	12.8	58.2	25	36	US-09-956-584-231127	Sequence 231127, A	C 391	12.6	57.3	25	26	US-09-660-080-1605	Sequence 1605, Ap
C 319	12.8	58.2	25	36	US-09-956-584-242034	Sequence 242034, A	C 392	12.6	57.3	25	26	US-09-660-080-1605	Sequence 1605, Ap
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C 322	12.8	58.2	25	36	US-09-956-584-264928	Sequence 264928, A	C 395	12.6	57.3	25	26	US-09-660-220-85019	Sequence 85019, A
C 323	12.8	58.2	25	36	US-09-956-604-69614	Sequence 69614, A	C 396	12.6	57.3	25	26	US-09-660-220-85019	Sequence 85019, A
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C 325	12.8	58.2	25	36	US-09-956-604-128772	Sequence 128772, A	C 398	12.6	57.3	25	29	US-09-745-317-15	Sequence 15, Appli
C 326	12.8	58.2	25	36	US-09-956-604-128772	Sequence 128772, A	C 399	12.6	57.3	25	29	US-09-745-317A-15	Sequence 15, Appli
C 327	12.8	58.2	25	36	US-09-956-604-69614	Sequence 69614, A	C 400	12.6	57.3	25	32	US-09-834-470-15	Sequence 15, Appli
C 328	12.8	58.2	25	36	US-09-956-604-69614	Sequence 69614, A	C 401	12.6	57.3	25	32	US-09-834-470-15	Sequence 15, Appli
C 329	12.8	58.2	25	36	US-09-956-604-128772	Sequence 128772, A	C 402	12.6	57.3	25	36	US-09-953-115-27469	Sequence 27469, A
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C 332	12.8	58.2	25	36	US-09-956-604B-69614	Sequence 69614, A	C 405	12.6	57.3	25	36	US-09-954-427-56630	Sequence 56630, A
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C 334	12.8	58.2	25	36	US-09-956-604B-128772	Sequence 128772, A	C 407	12.6	57.3	25	36	US-09-954-427-199323	Sequence 199323, A
C 335	12.8	58.2	25	67	US-60-233-166-29935	Sequence 29935, A	C 408	12.6	57.3	25	36	US-09-954-427-199323	Sequence 199323, A
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C 338	12.8	58.2	25	67	US-60-233-166-321612	Sequence 321612, A	C 411	12.6	57.3	25	36	US-09-954-427-201946	Sequence 201946, A
C 339	12.8	58.2	25	67	US-60-233-166-372310	Sequence 372310, A	C 412	12.6	57.3	25	36	US-09-954-427-201946	Sequence 201946, A
C 340	12.8	58.2	25	67	US-60-233-166-372310	Sequence 372310, A	C 413	12.6	57.3	25	36	US-09-954-427-246324	Sequence 246324, A
C 341	12.8	58.2	25	67	US-60-233-166-372328	Sequence 372328, A	C 414	12.6	57.3	25	36	US-09-954-427-246324	Sequence 246324, A
C 342	12.8	58.2	25	67	US-60-233-166-372328	Sequence 372328, A	C 415	12.6	57.3	25	36	US-09-954-427-351292	Sequence 351292, A
C 343	12.8	58.2	25	67	US-60-233-166-414094	Sequence 414094, A	C 416	12.6	57.3	25	36	US-09-954-427-351292	Sequence 351292, A
C 344	12.8	58.2	25	67	US-60-233-166-414094	Sequence 414094, A	C 417	12.6	57.3	25	36	US-09-956-584-61206	Sequence 61206, A
C 345	12.8	58.2	25	67	US-60-233-166-414094	Sequence 414094, A	C 418	12.6	57.3	25	36	US-09-956-584-61206	Sequence 61206, A
C 346	12.8	58.2	25	67	US-60-233-620-119613	Sequence 119613, A	C 419	12.6	57.3	25	36	US-09-956-584-61207	Sequence 61207, A
C 347	12.8	58.2	25	67	US-60-233-620-119613	Sequence 119613, A	C 420	12.6	57.3	25	36	US-09-956-584-61207	Sequence 61207, A
C 348	12.8	58.2	25	67	US-60-233-620-130471	Sequence 130471, A	C 421	12.6	57.3	25	36	US-09-956-584-127973	Sequence 127973, A
C 349	12.8	58.2	25	67	US-60-233-620-130471	Sequence 130471, A	C 422	12.6	57.3	25	36	US-09-956-584-127973	Sequence 127973, A
C 350	12.8	58.2	25	67	US-60-234-017-13032	Sequence 13032, A	C 423	12.6	57.3	25	36	US-09-956-584-144179	Sequence 144179, A
C 351	12.8	58.2	25	67	US-60-234-017-13032	Sequence 13032, A	C 424	12.6	57.3	25	36	US-09-956-584-144179	Sequence 144179, A
C 352	12.8	58.2	25	67	US-60-234-017-13043	Sequence 13043, A	C 425	12.6	57.3	25	36	US-09-956-584-144181	Sequence 144181, A
C 353	12.8	58.2	25	67	US-60-234-017-13043	Sequence 13043, A	C 426	12.6	57.3	25	36	US-09-956-584-144181	Sequence 144181, A
C 354	12.8	58.2	25	67	US-60-234-017-113658	Sequence 113658, A	C 427	12.6	57.3	25	36	US-09-956-584-144189	Sequence 144189, A
C 355	12.8	58.2	25	67	US-60-234-017-113658	Sequence 113658, A	C 428	12.6	57.3	25	36	US-09-956-584-144189	Sequence 144189, A
C 356	12.8	58.2	25	67	US-60-234-017-113665	Sequence 113665, A	C 429	12.6	57.3	25	36	US-09-956-584-144189	Sequence 144189, A
C 357	12.8	58.2	25	67	US-60-234-017-216390	Sequence 216390, A	C 430	12.6	57.3	25	36	US-09-956-584-203851	Sequence 203851, A
C 358	12.8	58.2	25	67	US-60-234-017-216390	Sequence 216390, A	C 431	12.6	57.3	25	36	US-09-956-584-380813	Sequence 380813, A
C 359	12.8	58.2	25	67	US-60-234-017-243858	Sequence 243858, A	C 432	12.6	57.3	25	36	US-09-956-584-380813	Sequence 380813, A
C 360	12.8	58.2	25	67	US-60-234-017-243858	Sequence 243858, A	C 433	12.6	57.3	25	36	US-09-956-584-518772	Sequence 518772, A
C 361	12.8	58.2	25	67	US-60-234-017-296877	Sequence 296877, A	C 434	12.6	57.3	25	36	US-09-956-584-518772	Sequence 518772, A
C 362	12.8	58.2	25	67	US-60-234-017-296877	Sequence 296877, A	C 435	12.6	57.3	25	36	US-09-956-584-593770	Sequence 593770, A
C 363	12.8	58.2	25	67	US-60-234-049-76342	Sequence 76342, A	C 436	12.6	57.3	25	36	US-09-956-604-22675	Sequence 22675, A
C 364	12.8	58.2	25	67	US-60-234-049-76342	Sequence 76342, A	C 437	12.6	57.3	25	36	US-09-956-604-22675	Sequence 22675, A
C 365	12.8	58.2	25	67	US-60-234-049-94045	Sequence 94045, A	C 438	12.6	57.3	25	36	US-09-956-604-22675	Sequence 22675, A
C 366	12.8	58.2	25	67	US-60-234-049-94045	Sequence 94045, A	C 439	12.6	57.3	25	36	US-09-956-604A-22675	Sequence 22675, A
C 367	12.8	58.2	25	67	US-60-353-987-75051	Sequence 75051, A	C 440	12.6	57.3	25	36	US-09-956-604A-22675	Sequence 22675, A
C 368	12.8	58.2	25	67	US-60-353-987-75051	Sequence 75051, A	C 441	12.6	57.3	25	36	US-09-956-604B-22675	Sequence 22675, A
C 369	12.8	58.2	25	79	US-60-353-987-509664	Sequence 509664, A	C 442	12.6	57.3	25	36	US-09-956-604B-22675	Sequence 22675, A
C 370	12.8	58.2	25	79	US-60-353-987-509664	Sequence 509664, A	C 443	12.6	57.3	25	41	US-10-170-332-15	Sequence 15, Appli
C 371	12.8	58.2	25	79	US-60-353-987-788258	Sequence 788258, A	C 444	12.6	57.3	25	41	US-10-170-332-15	Sequence 15, Appli
C 372	12.8	58.2	25	79	US-60-353-987-788258	Sequence 788258, A	C 445	12.6	57.3	25	67	US-60-233-166-56630	Sequence 56630, A
C 373	12.8	58.2	25	79	US-60-353-987-940701	Sequence 940701, A	C 446	12.6	57.3	25	67	US-60-233-166-56630	Sequence 56630, A
C 374	12.8	58.2	25	79	US-60-353-987-940701	Sequence 940701, A	C 447	12.6	57.3	25	67	US-60-233-166-199323	Sequence 199323, A
C 375	12.8	58.2	34	1	PCR-US99-20047-1	Sequence 1, Appli	C 448	12.6	57.3	25	67	US-60-233-166-199323	Sequence 199323, A
C 376	12.8	58.2	34	1	PCR-US99-20047-1	Sequence 1, Appli	C 449	12.6	57.3	25	67	US-60-233-166-201932	Sequence 201932, A
C 377	12.8	58.2	34	1	PCR-US99-20047-2	Sequence 2, Appli	C 450	12.6	57.3	25	67	US-60-233-166-201932	Sequence 201932, A
C 378	12.8	58.2	34	1	PCR-US99-20047-2	Sequence 2, Appli	C 451	12.6	57.3	25	67	US-60-233-166-201946	Sequence 201946, A
C 379	12.8	58.2	34	30	US-09-786-254-1	Sequence 1, Appli	C 452	12.6	57.3	25	67	US-60-233-166-201946	Sequence 201946, A
C 380	12.8	58.2	34	30	US-09-786-254-1	Sequence 1, Appli	C 453	12.6	57.3	25	67	US-60-233-166-246324	Sequence 246324, A
C 381	12.8	58.2	34	30	US-09-786-254-2	Sequence 2, Appli	C 454	12.6	57.3	25	67	US-60-233-166-246324	Sequence 246324, A
C 382	12.8	58.2	34	30	US-09-786-254-2	Sequence 2, Appli	C 455	12.6	57.3	25	67	US-60-233-166-351292	Sequence 351292, A
C 383	12.8	58.2	43	1	PCR-US99-20047-3	Sequence 3, Appli	C 456	12.6	57.3	25	67	US-60-233-166-351292	Sequence 351292, A
C 384	12.8	58.2	43	1	PCR-US99-20047-3	Sequence 3, Appli	C 457	12.6	57.3	25	67	US-60-233-620-33743	Sequence 33743, A
C 385	12.8	58.2	43	1	PCR-US99-20047-4	Sequence 4, Appli	C 458	12.6	57.3	25	67	US-60-233-620-33743	Sequence 33743, A
C 386	12.8	58.2	43	1	PCR-US99-20047-4	Sequence 4, Appli	C 459	12.6	57.3	25	67	US-60-233-620-33744	Sequence 33744, A

C 460	12.6	57.3	25	67	US-60-233-620-33744	Sequence 33744, A	533	12.4	56.4	25	26	US-09-660-220-114462	Sequence 114462,
C 461	12.6	57.3	25	67	US-60-233-620-99983	Sequence 99983, A	C 534	12.4	56.4	25	26	US-09-660-220-114463	Sequence 114463,
C 462	12.6	57.3	25	67	US-60-233-620-99983	Sequence 99983, A	C 535	12.4	56.4	25	26	US-09-660-220-114463	Sequence 114463,
C 463	12.6	57.3	25	67	US-60-233-620-128690	Sequence 128690, A	C 536	12.4	56.4	25	26	US-09-660-220-114463	Sequence 114463,
C 464	12.6	57.3	25	67	US-60-233-620-128690	Sequence 128690, A	C 537	12.4	56.4	25	26	US-09-660-220-114463	Sequence 114463,
C 465	12.6	57.3	25	67	US-60-233-620-128691	Sequence 128691, A	C 538	12.4	56.4	25	26	US-09-660-220-114463	Sequence 114463,
C 466	12.6	57.3	25	67	US-60-233-620-128691	Sequence 128691, A	C 539	12.4	56.4	25	26	US-09-660-220-114463	Sequence 114463,
C 467	12.6	57.3	25	67	US-60-234-017-23057	Sequence 23057, A	C 540	12.4	56.4	25	26	US-09-953-115-11189	Sequence 11189, A
C 468	12.6	57.3	25	67	US-60-234-017-23057	Sequence 23057, A	C 541	12.4	56.4	25	26	US-09-953-115-11189	Sequence 11189, A
C 469	12.6	57.3	25	67	US-60-234-017-23058	Sequence 23058, A	C 542	12.4	56.4	25	26	US-09-954-427-121041	Sequence 121041,
C 470	12.6	57.3	25	67	US-60-234-017-23058	Sequence 23058, A	C 543	12.4	56.4	25	26	US-09-954-427-121041	Sequence 121041,
C 471	12.6	57.3	25	67	US-60-234-017-82848	Sequence 82848, A	C 544	12.4	56.4	25	26	US-09-954-427-124080	Sequence 124080,
C 472	12.6	57.3	25	67	US-60-234-017-82848	Sequence 82848, A	C 545	12.4	56.4	25	26	US-09-954-427-131755	Sequence 131755,
C 473	12.6	57.3	25	67	US-60-234-017-161860	Sequence 161860, A	C 546	12.4	56.4	25	26	US-09-954-427-131755	Sequence 131755,
C 474	12.6	57.3	25	67	US-60-234-017-161860	Sequence 161860, A	C 547	12.4	56.4	25	26	US-09-954-427-203323	Sequence 203323,
C 475	12.6	57.3	25	67	US-60-234-017-161866	Sequence 161866, A	C 548	12.4	56.4	25	26	US-09-954-427-203323	Sequence 203323,
C 476	12.6	57.3	25	67	US-60-234-017-161866	Sequence 161866, A	C 549	12.4	56.4	25	26	US-09-954-427-203323	Sequence 203323,
C 477	12.6	57.3	25	67	US-60-234-017-161872	Sequence 161872, A	C 550	12.4	56.4	25	26	US-09-954-427-239525	Sequence 239525,
C 478	12.6	57.3	25	67	US-60-234-017-161872	Sequence 161872, A	C 551	12.4	56.4	25	26	US-09-954-427-239525	Sequence 239525,
C 479	12.6	57.3	25	67	US-60-234-017-205345	Sequence 205345, A	C 552	12.4	56.4	25	26	US-09-954-427-415703	Sequence 415703,
C 480	12.6	57.3	25	67	US-60-234-017-205345	Sequence 205345, A	C 553	12.4	56.4	25	26	US-09-956-584-12701	Sequence 12701, AP
C 481	12.6	57.3	25	67	US-60-234-017-364215	Sequence 364215, A	C 554	12.4	56.4	25	26	US-09-956-584-12701	Sequence 12701, AP
C 482	12.6	57.3	25	67	US-60-234-017-364215	Sequence 364215, A	C 555	12.4	56.4	25	26	US-09-956-584-39363	Sequence 39363, A
C 483	12.6	57.3	25	67	US-60-234-017-486871	Sequence 486871, A	C 556	12.4	56.4	25	26	US-09-956-584-39363	Sequence 39363, A
C 484	12.6	57.3	25	67	US-60-234-017-486871	Sequence 486871, A	C 557	12.4	56.4	25	26	US-09-956-584-63348	Sequence 63348, A
C 485	12.6	57.3	25	67	US-60-234-017-604091	Sequence 604091, A	C 558	12.4	56.4	25	26	US-09-956-584-63348	Sequence 63348, A
C 486	12.6	57.3	25	67	US-60-234-017-604091	Sequence 604091, A	C 559	12.4	56.4	25	26	US-09-956-584-66217	Sequence 66217, A
C 487	12.6	57.3	25	67	US-60-234-049-56620	Sequence 56620, A	C 560	12.4	56.4	25	26	US-09-956-584-66217	Sequence 66217, A
C 488	12.6	57.3	25	67	US-60-234-049-56620	Sequence 56620, A	C 561	12.4	56.4	25	26	US-09-956-584-88938	Sequence 88938, A
C 489	12.6	57.3	25	67	US-60-233-987-5941	Sequence 5941, AP	C 562	12.4	56.4	25	26	US-09-956-584-88938	Sequence 88938, A
C 490	12.6	57.3	25	67	US-60-233-987-5941	Sequence 5941, AP	C 563	12.4	56.4	25	26	US-09-956-584-88940	Sequence 88940, A
C 491	12.6	57.3	25	67	US-60-233-987-5942	Sequence 5942, AP	C 564	12.4	56.4	25	26	US-09-956-584-88940	Sequence 88940, A
C 492	12.6	57.3	25	67	US-60-233-987-5942	Sequence 5942, AP	C 565	12.4	56.4	25	26	US-09-956-584-93774	Sequence 93774, A
C 493	12.6	57.3	25	67	US-60-233-987-90478	Sequence 90478, A	C 566	12.4	56.4	25	26	US-09-956-584-93774	Sequence 93774, A
C 494	12.6	57.3	25	67	US-60-233-987-90478	Sequence 90478, A	C 567	12.4	56.4	25	26	US-09-956-584-109529	Sequence 109529, A
C 495	12.6	57.3	25	67	US-60-233-987-283495	Sequence 283495, A	C 568	12.4	56.4	25	26	US-09-956-584-109529	Sequence 109529, A
C 496	12.6	57.3	25	67	US-60-233-987-283495	Sequence 283495, A	C 569	12.4	56.4	25	26	US-09-956-584-131800	Sequence 131800, A
C 497	12.6	57.3	25	67	US-60-233-987-297457	Sequence 297457, A	C 570	12.4	56.4	25	26	US-09-956-584-131800	Sequence 131800, A
C 498	12.6	57.3	25	67	US-60-233-987-297457	Sequence 297457, A	C 571	12.4	56.4	25	26	US-09-956-584-136425	Sequence 136425, A
C 499	12.6	57.3	25	67	US-60-233-987-337874	Sequence 337874, A	C 572	12.4	56.4	25	26	US-09-956-584-136425	Sequence 136425, A
C 500	12.6	57.3	25	67	US-60-233-987-337874	Sequence 337874, A	C 573	12.4	56.4	25	26	US-09-956-584-207883	Sequence 207883, A
C 501	12.6	57.3	25	67	US-60-233-987-540297	Sequence 540297, A	C 574	12.4	56.4	25	26	US-09-956-584-207883	Sequence 207883, A
C 502	12.6	57.3	25	67	US-60-233-987-540297	Sequence 540297, A	C 575	12.4	56.4	25	26	US-09-956-584-226472	Sequence 226472, A
C 503	12.6	57.3	25	67	US-60-233-987-564953	Sequence 564953, A	C 576	12.4	56.4	25	26	US-09-956-584-226472	Sequence 226472, A
C 504	12.6	57.3	25	67	US-60-233-987-564953	Sequence 564953, A	C 577	12.4	56.4	25	26	US-09-956-584-226473	Sequence 226473, A
C 505	12.6	57.3	25	67	US-60-233-987-639291	Sequence 639291, A	C 578	12.4	56.4	25	26	US-09-956-584-226473	Sequence 226473, A
C 506	12.6	57.3	25	67	US-60-233-987-639291	Sequence 639291, A	C 579	12.4	56.4	25	26	US-09-956-584-226474	Sequence 226474, A
C 507	12.6	57.3	25	67	US-60-233-987-735589	Sequence 735589, A	C 580	12.4	56.4	25	26	US-09-956-584-226474	Sequence 226474, A
C 508	12.6	57.3	25	67	US-60-233-987-735589	Sequence 735589, A	C 581	12.4	56.4	25	26	US-09-956-584-295609	Sequence 295609, A
C 509	12.6	57.3	25	67	US-60-233-987-887212	Sequence 887212, A	C 582	12.4	56.4	25	26	US-09-956-584-295609	Sequence 295609, A
C 510	12.6	57.3	25	67	US-60-233-987-887212	Sequence 887212, A	C 583	12.4	56.4	25	26	US-09-956-584-340514	Sequence 340514, A
C 511	12.6	57.3	25	67	US-60-233-987-898442	Sequence 898442, A	C 584	12.4	56.4	25	26	US-09-956-584-340514	Sequence 340514, A
C 512	12.6	57.3	25	67	US-60-233-987-898442	Sequence 898442, A	C 585	12.4	56.4	25	26	US-09-956-584-392203	Sequence 392203, A
C 513	12.6	57.3	25	67	US-60-233-987-898442	Sequence 898442, A	C 586	12.4	56.4	25	26	US-09-956-584-392203	Sequence 392203, A
C 514	12.6	57.3	25	67	US-60-233-987-899706	Sequence 899706, A	C 587	12.4	56.4	25	26	US-09-956-584-418163	Sequence 418163, A
C 515	12.6	57.3	25	67	US-60-233-987-899706	Sequence 899706, A	C 588	12.4	56.4	25	26	US-09-956-584-418163	Sequence 418163, A
C 516	12.6	57.3	50	1	PCT-US01-47856-2060	Sequence 2060, AP	C 589	12.4	56.4	25	26	US-09-956-584-418171	Sequence 418171, A
C 517	12.6	57.3	50	40	US-10-131-827-2060	Sequence 2060, AP	C 590	12.4	56.4	25	26	US-09-956-584-418171	Sequence 418171, A
C 518	12.6	57.3	50	40	US-10-131-827-2060	Sequence 2060, AP	C 591	12.4	56.4	25	26	US-09-956-584-86954	Sequence 86954, A
C 519	12.6	57.3	50	40	US-10-131-831-2060	Sequence 2060, AP	C 592	12.4	56.4	25	26	US-09-956-584-86954	Sequence 86954, A
C 520	12.6	57.3	50	40	US-10-131-831-2060	Sequence 2060, AP	C 593	12.4	56.4	25	26	US-09-956-584-86957	Sequence 86957, A
C 521	12.4	56.4	20	16	US-09-201-228A-5711	Sequence 5711, AP	C 594	12.4	56.4	25	26	US-09-956-584-86957	Sequence 86957, A
C 522	12.4	56.4	20	16	US-09-201-228A-5711	Sequence 5711, AP	C 595	12.4	56.4	25	26	US-09-956-584-86990	Sequence 86990, A
C 523	12.4	56.4	21	16	US-09-284-725-33	Sequence 725, AP	C 596	12.4	56.4	25	26	US-09-956-584-86990	Sequence 86990, A
C 524	12.4	56.4	21	16	US-09-284-725-33	Sequence 725, AP	C 597	12.4	56.4	25	26	US-09-956-584-86990	Sequence 86990, A
C 525	12.4	56.4	21	16	US-10-263-594-33	Sequence 33, AP	C 598	12.4	56.4	25	26	US-09-956-584-86994	Sequence 86994, A
C 526	12.4	56.4	21	43	US-10-263-594-33	Sequence 33, AP	C 599	12.4	56.4	25	26	US-09-956-584-86994	Sequence 86994, A
C 527	12.4	56.4	25	26	US-09-660-080-10272	Sequence 10272, A	C 600	12.4	56.4	25	26	US-09-956-584-86997	Sequence 86997, A
C 528	12.4	56.4	25	26	US-09-660-080-10272	Sequence 10272, A	C 601	12.4	56.4	25	26	US-09-956-584-86990	Sequence 86990, A
C 529	12.4	56.4	25	26	US-09-660-220-62449	Sequence 62449, A	C 602	12.4	56.4	25	26	US-09-956-584-86990	Sequence 86990, A
C 530	12.4	56.4	25	26	US-09-660-220-62449	Sequence 62449, A	C 603	12.4	56.4	25	26	US-09-956-584-86994	Sequence 86994, A
C 531	12.4	56.4	25	26	US-09-660-220-62455	Sequence 62455, A	C 604	12.4	56.4	25	26	US-09-956-584-86994	Sequence 86994, A
C 532	12.4	56.4	25	26	US-09-660-220-62455	Sequence 62455, A	C 605	12.4	56.4	25	26	US-09-956-584-86997	Sequence 86997, A

C 606	12.4	56.4	25	36	US-09-956-604B-86957	Sequence 86957, A	679	12.4	56.4	25	79	US-60-353-987-387487	Sequence 387487, A
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STRANDEDNESS: single-stranded
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: cDNA to mRNA
HYPOTHETICAL: no
ANTI-SENSE: yes
FRAGMENT TYPE:
ORIGINAL SOURCE:
IMMEDIATE SOURCE:
POSITION IN GENOME:
FEATURE:
PUBLICATION INFORMATION:
US-09-056-363-1

Query Match          100.0%; Score 22; DB 14; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGAGACCGATATCGGTCTCAG 22
Db 1 CTGAGACCGATATCGGTCTCAG 22

RESULT 2
US-09-056-363-1/c
; Sequence 1, Application US/09056363
; GENERAL INFORMATION:
; APPLICANT: Goodwin et al.
; TITLE OF INVENTION: Production of Functional Proteins:
; TITLE OF INVENTION: Balance of Shear Stress and Gravity
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James M. Cate, NASA Johnson Space Center
; STREET: 2101 NASA Road 1, Mail code: HA
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77058-3696
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 Mb floppy disk
; COMPUTER: PC
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Microsoft Word for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/056,363
; FILING DATE: April 7, 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/043,205
; FILING DATE: April 8, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: James M. Cate
; REGISTRATION NUMBER: 25,181
; REFERENCE/DOCKET NUMBER: MSC-22859-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (281)483-1001
; TELEFAX: (281)244-8452
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 bp
; TYPE: nucleic acid
; STRANDEDNESS: single-stranded
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: cDNA to mRNA
; HYPOTHETICAL: no
; ANTI-SENSE: yes
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; IMMEDIATE SOURCE:
; POSITION IN GENOME:
; FEATURE:
; PUBLICATION INFORMATION:
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US-09-056-363-1

Query Match          100.0%; Score 22; DB 14; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGAGACCGATATCGGTCTCAG 22
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RESULT 3
US-09-532-001-1
; Sequence 1, Application US/09532001
; GENERAL INFORMATION:
; APPLICANT: Goodwin et al.
; TITLE OF INVENTION: Production of Functional Proteins:
; TITLE OF INVENTION: Balance of Shear Stress and Gravity
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James M. Cate, NASA Johnson Space Center
; STREET: 2101 NASA Road 1, Mail code: HA
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77058-3696
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 Mb floppy disk
; COMPUTER: PC
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Microsoft Word for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/532,001
; FILING DATE: 21-Mar-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/056,363
; FILING DATE: April 7, 1998
; APPLICATION NUMBER: 60/043,205
; FILING DATE: April 8, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: James M. Cate
; REGISTRATION NUMBER: 25,181
; REFERENCE/DOCKET NUMBER: MSC-22859-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (281)483-1001
; TELEFAX: (281)244-8452
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 bp
; TYPE: nucleic acid
; STRANDEDNESS: single-stranded
; TOPOLOGY: linear
; MOLECULE TYPE: <Unknown>
; DESCRIPTION: cDNA to mRNA
; HYPOTHETICAL: no
; ANTI-SENSE: yes
; FRAGMENT TYPE: <Unknown>
; ORIGINAL SOURCE:
; IMMEDIATE SOURCE:
; POSITION IN GENOME:
; FEATURE:
; PUBLICATION INFORMATION:
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
;
US-09-532-001-1

Query Match          100.0%; Score 22; DB 20; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGAGACCGATATCGGTCTCAG 22
Db 1 CTGAGACCGATATCGGTCTCAG 22
```

RESULT 4
US-09-532-001-1/c
Sequence 1, Application US/09532001
GENERAL INFORMATION:
APPLICANT: Goodwin et al.
TITLE OF INVENTION: Production of Functional Proteins:
Balance of Shear Stress and Gravity
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: James M. Cate, NASA Johnson Space Center
STREET: 2101 NASA Road 1, Mail code: HA
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77058-3696
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 Mb floppy disk
COMPUTER: PC
OPERATING SYSTEM: Windows 95
SOFTWARE: Microsoft Word for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/532.001
FILING DATE: 21-Mar-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/056,363
FILING DATE: April 7, 1998
APPLICATION NUMBER: 60/043,205
FILING DATE: April 8, 1997
ATTORNEY/AGENT INFORMATION:
NAME: James M. Cate
REGISTRATION NUMBER: 25,181
REFERENCE/DOCKET NUMBER: MSC-22859-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (281)483-1001
TELEFAX: (281)244-8452
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 22 bp
TYPE: nucleic acid
STRANDEDNESS: single-stranded
TOPOLOGY: linear
MOLECULE TYPE: <Unknown>
DESCRIPTION: cDNA to mRNA
HYPOTHETICAL: no
ANTI-SENSE: yes
FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:
IMMEDIATE SOURCE:
POSITION IN GENOME:
FEATURE:
PUBLICATION INFORMATION:
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-532-001-1

Query Match 100.0%; Score 22; DB 20; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTGAGACCGATATCGGTCTCAG 22
DB 22 CTGAGACCGATATCGGTCTCAG 1

RESULT 5
US-09-584-245934
Sequence 245934, Application US/09565584
GENERAL INFORMATION:
APPLICANT: Miltman, Michael
TITLE OF INVENTION: Methods of Genetic Analysis of Mus Musculus
FILE REFERENCE: 3115.1

CURRENT APPLICATION NUMBER: US/09/956,584
CURRENT FILING DATE: 2001-09-19
PRIOR APPLICATION NUMBER: 60/234,017
PRIOR FILING DATE: 2000-09-20
NUMBER OF SEQ ID NOS: 605887
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 245934
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-09-584-245934

Query Match 71.8%; Score 15.8; DB 36; Length 25;
Best Local Similarity 89.5%; Pred. No. 7.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 AGACCGATATCGGTCTCAG 22
DB 6 AGACCGATATCGGTCTCAG 24

RESULT 6
US-09-584-245934/c
Sequence 245934, Application US/09565584
GENERAL INFORMATION:
APPLICANT: Miltman, Michael
TITLE OF INVENTION: Methods of Genetic Analysis of Mus Musculus
FILE REFERENCE: 3115.1
CURRENT APPLICATION NUMBER: US/09/956,584
CURRENT FILING DATE: 2001-09-19
PRIOR APPLICATION NUMBER: 60/234,017
PRIOR FILING DATE: 2000-09-20
NUMBER OF SEQ ID NOS: 605887
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 245934
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-09-584-245934

Query Match 71.8%; Score 15.8; DB 36; Length 25;
Best Local Similarity 89.5%; Pred. No. 7.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CTGAGACCGATATCGGTCT 19
DB 24 CAGAGACCGATACCGGTCT 6

RESULT 7
US-60-234-017-201611
Sequence 201611, Application US/60234017
GENERAL INFORMATION:
APPLICANT: Miltman, M
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis of Mus
FILE REFERENCE: 3115
CURRENT APPLICATION NUMBER: US/60/234,017
CURRENT FILING DATE: 2000-09-20
NUMBER OF SEQ ID NOS: 605887
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 201611
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: GenBank AA823028
US-60-234-017-201611

Query Match 71.8%; Score 15.8; DB 67; Length 25;
Best Local Similarity 89.5%; Pred. No. 7.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 AGACCGATATCGGCTCAG 22
6 AGACCGGATATCGGCTCTG 24

```

RESULT 8
US-60-234-017-201611/c
Sequence 201611, Application US/60234017
GENERAL INFORMATION:
APPLICANT: Miltman, M
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis of Mus
TITLE OF INVENTION: musculus
FILE REFERENCE: 3115
CURRENT APPLICATION NUMBER: US/60/234, 017
CURRENT FILING DATE: 2000-09-20
NUMBER OF SEQ ID NOS: 605887
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 201611
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: GenBank AA823028
US-60-234-017-201611

```

Query Match	71.8%	Score 15.8	DB 67	Length 25
Best Local Similarity	89.5%	Pred. No. 7.8e+02		
Matches 17; Conservative	0	Mismatches 2	Indels 0	Gaps 0

QY • 1 CTGAGACCGATATCGGTCT 19
Db 24 CAGAGACCGATACCGGTCT 6

```

RESULT 9
US-60-353-987-403951
; Sequence 403951, Application US/60353987
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-UI33
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/60/353,987
; CURRENT FILING DATE: 1992-02-01
; NUMBER OF SEQ. ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 403951
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-60-353-987-403951

```

Query Match	67.3%	Score 14.8;	DB 79;	Length 25;
Best Local Similarity	88.9%;	Pred. No. 2.7e+03;		
Matches 16;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;

[illegible]

```

RESULT 10
US-60-353-987-403951/c
Sequence 403951, Application US/60353987
GENERAL INFORMATION:
APPLICANT: Miltmann, Michael
TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
FILE REFERENCE: 3121
CURRENT APPLICATION NUMBER: US/60/353,987
CURRENT FILING DATE: 2002-02-01
NUMBER OF SEQ. ID NOS. 997516
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

```

```

; SEQ ID NO 403951
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-60-353-987-403951

```

Query Match	67.3%	Score 14.8;	DB 79;	Length 25;
Best Local Similarity	88.9%	Pred. No. 2.7e+03;		
Matches 16;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;

QY 3 GAGACCGATATCGGTC 20
| | | | | | | | | |
Db 19 GGGACCGATGTCGGTCTC 2

```

US-09-954-427-371667
RESULT 11
US-09-954-427-371667
Sequence 371667, Application US/09954427
GENERAL INFORMATION:
APPLICANT: Miltmann
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
TITLE OF INVENTION: Genome
FILE REFERENCE: 3112
CURRENT APPLICATION NUMBER: US/09/954,427
CURRENT FILING DATE: 2001-09-17
NUMBER OF SEQ ID NOS: 420507
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 371667
LENGTH: 25
TYPE: DNA
ORGANISM: Rattus norvegicus
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: GenBank X92070
US-09-954-427-371667

```

Query Match	66.4%	Score 14.6;	DB 36;	Length 25;
Best Local Similarity	81.0%	Pred. No. 3.5e+03;		
Matches 17; Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0;

QY	2	TGAGACCGATATCGGTC	22
Db	5	TGAGACTGACCCCGGCTCAG	25

RESULT 12
 US-09-954-427-371667/c
 : Sequence 371667, Application US/0954427
 : GENERAL INFORMATION:
 : APPLICANT: Miltmann
 : APPLICANT: Affymetrix, Inc.
 : TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
 : TITLE OF INVENTION: Genome
 : FILE REFERENCE: 3112
 : CURRENT APPLICATION NUMBER: US/09/954,427
 : CURRENT FILING DATE: 2001-09-17
 : NUMBER OF SEQ ID NOS: 420907
 : SOFTWARE: FastSeq for Windows Version 4.0
 : SEQ ID NO 371667
 : LENGTH: 25
 : TYPE: DNA
 : ORGANISM: Rattus norvegicus
 : PUBLICATION INFORMATION:
 : DATABASE ACCESSION NUMBER: GenBank X92070
 US-09-954-427-371667

Query Match	66.4%	Score 14.6;	DB 36;	Length 25;
Best Local Similarity	81.0%;	Pred. No. 3.5e+03;		
Matches 17;	Conservative 0;	Mismatches 4;	Indels 0;	Gaps 0;

QY	1	CTGAGACCGATATCGGTCTCA	21
Db	25	CTGAGACCGGGGTCACTCTCA	5

```
RESULT 13
US-09-954-429A-18545
; Sequence 18545, Application US/09954429A
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat Neurobiology
; FILE REFERENCE: 3114.1
; CURRENT APPLICATION NUMBER: US/09/954,429A
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: 60/233,357
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 21305
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 18545
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-09-954-429A-18545

Query Match      66.4%; Score 14.6; DB 36; Length 25;
Best Local Similarity 81.0%; Pred. No. 3.5e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2 TGAGACCGGATATCGGTCTCAG 22
DB      5 TGAGACTGACCCCGGTCTCAG 25

RESULT 14
US-09-954-429A-18545/c
; Sequence 18545, Application US/09954429A
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat Neurobiology
; FILE REFERENCE: 3114.1
; CURRENT APPLICATION NUMBER: US/09/954,429A
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: 60/233,357
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 21305
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 18545
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-09-954-429A-18545

Query Match      66.4%; Score 14.6; DB 36; Length 25;
Best Local Similarity 81.0%; Pred. No. 3.5e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 CTGAGACCGATATCGGTCTCA 21
DB      25 CTGAGACCGGGGTCTCAGTCTCA 5

RESULT 15
US-60-233-166-371667
; Sequence 371667, Application US/60233166
; GENERAL INFORMATION:
; APPLICANT: Miltmann
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/60/233,166
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 371667
; LENGTH: 25
```

```
TYPE: DNA
ORGANISM: Rattus norvegicus
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: GenBank X92070
US-60-233-166-371667

Query Match      66.4%; Score 14.6; DB 67; Length 25;
Best Local Similarity 81.0%; Pred. No. 3.5e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2 TGAGACCGGATATCGGTCTCAG 22
DB      5 TGAGACTGACCCCGGTCTCAG 25

RESULT 16
US-60-233-166-371667/c
; Sequence 371667, Application US/60233166
; GENERAL INFORMATION:
; APPLICANT: Miltmann
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/60/233,166
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 371667
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: GenBank X92070
US-60-233-166-371667

Query Match      66.4%; Score 14.6; DB 67; Length 25;
Best Local Similarity 81.0%; Pred. No. 3.5e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 CTGAGACCGATATCGGTCTCA 21
DB      25 CTGAGACCGGGGTCTCAGTCTCA 5

RESULT 17
US-60-233-357-20470
; Sequence 20470, Application US/60233357
; GENERAL INFORMATION:
; APPLICANT: Miltmann
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3114
; CURRENT APPLICATION NUMBER: US/60/233,357
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 21305
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20470
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: GenBank X92070
US-60-233-357-20470

Query Match      66.4%; Score 14.6; DB 67; Length 25;
Best Local Similarity 81.0%; Pred. No. 3.5e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2 TGAGACCGGATATCGGTCTCAG 22
DB      5 TGAGACTGACCCCGGTCTCAG 25
```

```
RESULT 18
US-60-233-357-20470/c
; Sequence 20470, Application US/60233357
; GENERAL INFORMATION:
; APPLICANT: Miltmann
; TITLE OF INVENTION: Methode of Genetic Analysis of Rat
; FILE REFERENCE: 3114
; CURRENT APPLICATION NUMBER: US/60/233,357
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 21305
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20470
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank X92070
US-60-233-357-20470

Query Match
Best Local Similarity 66.4%; Score 14.6; DB 67; Length 25;
Best Local Similarity 81.0%; Pred. No. 3.5e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CTGAGACCGGATATCGCTCTCA 21
Db 25 CTGAGACCGGCGGTCTCTCA 5

RESULT 19
US-60-233-620-99732
; Sequence 99732, Application US/60233620
; GENERAL INFORMATION:
; APPLICANT: Miltmann
; TITLE OF INVENTION: Methode of Genetic Analysis of
; FILE REFERENCE: 3116
; CURRENT APPLICATION NUMBER: US/60/233,620
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 131820
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 99732
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AF069497
US-60-233-620-99732

Query Match
Best Local Similarity 66.4%; Score 14.6; DB 67; Length 25;
Best Local Similarity 81.0%; Pred. No. 3.5e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CTGAGACCGGATATCGCTCTCA 21
Db 4 CCGATACAGATATAGGTCTCA 24

RESULT 20
US-60-233-620-99732/c
; Sequence 99732, Application US/60233620
; GENERAL INFORMATION:
; APPLICANT: Miltmann
; TITLE OF INVENTION: Methode of Genetic Analysis of
; FILE REFERENCE: 3116
; CURRENT APPLICATION NUMBER: US/60/233,620
; CURRENT FILING DATE: 2000-10-24
```

```
; NUMBER OF SEQ ID NOS: 131820
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 99732
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AF069497
US-60-233-620-99732

Query Match
Best Local Similarity 66.4%; Score 14.6; DB 67; Length 25;
Best Local Similarity 81.0%; Pred. No. 3.5e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 TGAGACCGGATATCGCTCTCAG 22
Db 24 TGAGACCGGATATCGCTCTCAG 4

RESULT 21
US-09-956-584-216321
; Sequence 216321, Application US/09956584
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus Musculus
; FILE REFERENCE: 3115.1
; CURRENT APPLICATION NUMBER: US/09/956,584
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,017
; PRIOR FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 216321
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-956-584-216321

Query Match
Best Local Similarity 65.5%; Score 14.4; DB 36; Length 25;
Best Local Similarity 93.8%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GACCGAATATCGCTCTC 20
Db 5 GACCGAATATCGCTCTC 20

RESULT 22
US-09-956-584-216321/c
; Sequence 216321, Application US/09956584
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus Musculus
; FILE REFERENCE: 3115.1
; CURRENT APPLICATION NUMBER: US/09/956,584
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,017
; PRIOR FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 216321
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-956-584-216321

Query Match
Best Local Similarity 65.5%; Score 14.4; DB 36; Length 25;
Best Local Similarity 93.8%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GAGACCGGATATCGCTC 18
Db 20 GAGACCGGATATCGCTC 5
```

RESULT 23
US-60-234-017-216691
; Sequence 216691, Application US/60234017
; GENERAL INFORMATION:
; APPLICANT: Miltmann, M
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus
; FILE REFERENCE: 3115
; CURRENT APPLICATION NUMBER: US/60/234,017
; CURRENT FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 216691
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Genbank AT789011
US-60-234-017-216691
Query Match 65.5%; Score 14.4; DB 67; Length 25;
Best Local Similarity 93.8%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 5 GACCGATATCGGTCTC 20
Db 5 GACCGAATCGGTCTC 20
RESULT 24
US-60-234-017-216691/c
; Sequence 216691, Application US/60234017
; GENERAL INFORMATION:
; APPLICANT: Miltmann, M
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus
; FILE REFERENCE: 3115
; CURRENT APPLICATION NUMBER: US/60/234,017
; CURRENT FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 216691
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Genbank AT789011
US-60-234-017-216691
Query Match 65.5%; Score 14.4; DB 67; Length 25;
Best Local Similarity 93.8%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 3 GAGACCGATATCGGTCTC 18
Db 20 GAGACCGATATCGGTCTC 5
RESULT 25
US-60-353-987-90477
; Sequence 90477, Application US/60353987
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/60/353,987
; CURRENT FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 90477
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-60-353-987-90477
Query Match 64.5%; Score 14.2; DB 79; Length 25;
Best Local Similarity 84.2%; Pred. No. 5.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 3 GAGACCGATATCGGTCTCA 21
Db 6 GAGACCGATATCGGTATGA 24
RESULT 26
US-60-353-987-90477/c
; Sequence 90477, Application US/60353987
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/60/353,987
; CURRENT FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 90477
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-60-353-987-90477
Query Match 64.5%; Score 14.2; DB 79; Length 25;
Best Local Similarity 84.2%; Pred. No. 5.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 2 TGAGACCGATATCGGTCTC 20
Db 24 TCATACCGATATGGGTCTC 6

RESULT 27
PCT-US99-10361-32
; Sequence 32, Application PC/TUS9910361
; GENERAL INFORMATION:
; APPLICANT: ISIS Pharmaceuticals, Inc. et al.
; FILE REFERENCE: IBIS-0144
; CURRENT APPLICATION NUMBER: PCT/US99/10361
; CURRENT FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 32
; LENGTH: 28
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic RNA molecule
PCT-US99-10361-32
Query Match 64.5%; Score 14.2; DB 1; Length 28;
Best Local Similarity 68.4%; Pred. No. 5.7e+03;
Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
OY 3 GAGACCGATATCGGTCTCA 21
Db 1 GAGACCCAAUUCUGUCUCA 19
RESULT 28
PCT-US99-10361-32/c
; Sequence 32, Application PC/TUS9910361
; GENERAL INFORMATION:
; APPLICANT: ISIS Pharmaceuticals, Inc. et al.

```

; TITLE OF INVENTION: Modulation Of Molecular Interaction Sites On RNA And Other Biomo
; FILE REFERENCE: IBIS-014
; CURRENT APPLICATION NUMBER: PCT/US99/10361
; CURRENT FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 32
; LENGTH: 28
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic RNA molecule
PCT-US99-10361-32

Query Match          64.5%; Score 14.2; DB 1; Length 28;
Best Local Similarity 84.2%; Pred. No. 5.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TGAGACCGATATCGGTCTC 20
    ||||| ||||| |||||
Db 19 TGAGACAGATTGGGTCTC 1

RESULT 29
; Sequence 30, Application US/09310735
; GENERAL INFORMATION:
; APPLICANT: Ecker, David J
; APPLICANT: Grifley, Richard
; APPLICANT: Crooke, Stanley T
; APPLICANT: Sampath, Ranga
; APPLICANT: Swayze, Eric
; APPLICANT: Mohan, Venkatraman
; APPLICANT: Hofstadler, Steven
; APPLICANT: McNeill, John
; TITLE OF INVENTION: Modulation of Molecular Interaction Sites on RNA and
; FILE REFERENCE: IBIS0015
; CURRENT APPLICATION NUMBER: US/09/310,735
; CURRENT FILING DATE: 1999-05-12
; PRIOR APPLICATION NUMBER: 09/076,404
; PRIOR FILING DATE: 1998-05-12
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 28
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Novel Sequence
US-09-310-735-30

Query Match          64.5%; Score 14.2; DB 17; Length 28;
Best Local Similarity 68.4%; Pred. No. 5.7e+03;
Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 GAGACCGATATCGGTCTCA 21
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Db 1 GAGACCCCAAUUCUGUCUCA 19

RESULT 30
US-09-310-735-30/c
; Sequence 30, Application US/09310735
; GENERAL INFORMATION:
; APPLICANT: Ecker, David J
; APPLICANT: Grifley, Richard
; APPLICANT: Crooke, Stanley T
; APPLICANT: Sampath, Ranga
; APPLICANT: Swayze, Eric
; APPLICANT: Mohan, Venkatraman
; APPLICANT: Hofstadler, Steven
; APPLICANT: McNeill, John
; TITLE OF INVENTION: Modulation of Molecular Interaction Sites on RNA and
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; TITLE OF INVENTION: Other Biomolecules
; FILE REFERENCE: IBIS0015
; CURRENT APPLICATION NUMBER: US/09/310,735
; CURRENT FILING DATE: 1999-05-12
; PRIOR APPLICATION NUMBER: 09/076,404
; PRIOR FILING DATE: 1998-05-12
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 28
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Novel Sequence
US-09-310-735-30

Query Match          64.5%; Score 14.2; DB 17; Length 28;
Best Local Similarity 84.2%; Pred. No. 5.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TGAGACCGATATCGGTCTC 20
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Db 19 TGAGACAGATTGGGTCTC 1

RESULT 31
US-09-310-735A-30
; Sequence 30, Application US/09310735A
; GENERAL INFORMATION:
; APPLICANT: Ecker, David J
; APPLICANT: Grifley, Richard
; APPLICANT: Crooke, Stanley T
; APPLICANT: Sampath, Ranga
; APPLICANT: Swayze, Eric
; APPLICANT: Mohan, Venkatraman
; APPLICANT: Hofstadler, Steven
; APPLICANT: McNeill, John
; TITLE OF INVENTION: Modulation of Molecular Interaction Sites on RNA and
; FILE REFERENCE: IBIS0015
; CURRENT APPLICATION NUMBER: US/09/310,735A
; CURRENT FILING DATE: 1999-05-12
; PRIOR APPLICATION NUMBER: 09/076,404
; PRIOR FILING DATE: 1998-05-12
; NUMBER OF SEQ ID NOS: 393
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 28
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Novel Sequence
US-09-310-735A-30

Query Match          64.5%; Score 14.2; DB 17; Length 28;
Best Local Similarity 68.4%; Pred. No. 5.7e+03;
Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 GAGACCGATATCGGTCTCA 21
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Db 1 GAGACCCCAAUUCUGUCUCA 19

RESULT 32
US-09-310-735A-30/c
; Sequence 30, Application US/09310735A
; GENERAL INFORMATION:
; APPLICANT: Ecker, David J
; APPLICANT: Grifley, Richard
; APPLICANT: Crooke, Stanley T
; APPLICANT: Sampath, Ranga
; APPLICANT: Swayze, Eric
; APPLICANT: Mohan, Venkatraman
```

```

; APPLICANT: Hofstadler, Steven
; APPLICANT: McNeill, John
; TITLE OF INVENTION: Modulation of Molecular Interaction Sites on RNA and
; FILE REFERENCE: IBIS0015
; CURRENT APPLICATION NUMBER: US/09/310,735A
; CURRENT FILING DATE: 1999-05-12
; PRIOR APPLICATION NUMBER: 09/076,404
; PRIOR FILING DATE: 1998-05-12
; NUMBER OF SEQ ID NOS: 393
; SOFTWARE: PatentIn Ver. 2.1
; LENGTH: 28
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Novel Sequence
US-09-310-735A-30

Query Match      64.5%; Score 14.2; DB 17; Length 28;
Best Local Similarity 84.2%; Pred. No. 5.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 TGAGACCGATATCGGTCTC 20
Db      19 TGAGACAGATTGGGTCTC 1

RESULT 33
US-09-310-735C-30
; Sequence 30, Application US/09310735C
; GENERAL INFORMATION:
; APPLICANT: Ecker, David J
; APPLICANT: Griffey, Richard
; APPLICANT: Crooke, Stanley T
; APPLICANT: Swayze, Ranga
; APPLICANT: Swayze, Eric
; APPLICANT: Mohan, Venkatreman
; APPLICANT: Hofstadler, Steven
; APPLICANT: McNeill, John
; TITLE OF INVENTION: Modulation of Molecular Interaction Sites on RNA and
; FILE REFERENCE: IBIS0015
; CURRENT APPLICATION NUMBER: US/09/310,735C
; CURRENT FILING DATE: 1999-05-12
; PRIOR APPLICATION NUMBER: 09/076,404
; PRIOR FILING DATE: 1998-05-12
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 28
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Novel Sequence
US-09-310-735C-30

Query Match      64.5%; Score 14.2; DB 17; Length 28;
Best Local Similarity 68.4%; Pred. No. 5.7e+03;
Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy      3 GAGACCGATATCGGTCTCA 21
Db      1 GAGACCCAAUUCUGUCUCA 19

RESULT 34
US-09-310-735C-30/C
; Sequence 30, Application US/09310735C
; GENERAL INFORMATION:
; APPLICANT: Ecker, David J
; APPLICANT: Griffey, Richard
; APPLICANT: Crooke, Stanley T
```

```

; APPLICANT: Sampath, Ranga
; APPLICANT: Swayze, Eric
; APPLICANT: Mohan, Venkatreman
; APPLICANT: Hofstadler, Steven
; APPLICANT: McNeill, John
; TITLE OF INVENTION: Modulation of Molecular Interaction Sites on RNA and
; FILE REFERENCE: IBIS0015
; CURRENT APPLICATION NUMBER: US/09/310,735C
; CURRENT FILING DATE: 1999-05-12
; PRIOR APPLICATION NUMBER: 09/076,404
; PRIOR FILING DATE: 1998-05-12
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 28
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Novel Sequence
US-09-310-735C-30

Query Match      64.5%; Score 14.2; DB 17; Length 28;
Best Local Similarity 84.2%; Pred. No. 5.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 TGAGACCGATATCGGTCTC 20
Db      19 TGAGACAGATTGGGTCTC 1

RESULT 35
US-09-310-761-30
; Sequence 30, Application US/09310761
; GENERAL INFORMATION:
; APPLICANT: Ecker, David J
; APPLICANT: Griffey, Richard
; APPLICANT: Crooke, Stanley T
; APPLICANT: Sampath, Ranga
; APPLICANT: Mohan, Venkatreman
; APPLICANT: Swayze, Eric
; APPLICANT: Hofstadler, Steven
; APPLICANT: McNeill, John
; TITLE OF INVENTION: RNA And Methods Of Modulating The Same
; FILE REFERENCE: IBIS0170
; CURRENT APPLICATION NUMBER: US/09/310,761
; CURRENT FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 28
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Novel Sequence
US-09-310-761-30

Query Match      64.5%; Score 14.2; DB 17; Length 28;
Best Local Similarity 68.4%; Pred. No. 5.7e+03;
Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy      3 GAGACCGATATCGGTCTCA 21
Db      1 GAGACCCAAUUCUGUCUCA 19

RESULT 36
US-09-310-761-30/C
; Sequence 30, Application US/09310761
; GENERAL INFORMATION:
; APPLICANT: Ecker, David J
; APPLICANT: Griffey, Richard
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; APPLICANT: Crooke, Stanley T
; APPLICANT: Sampath, Ranga
; APPLICANT: Mohan, Venkatraman
; APPLICANT: Swayze, Eric
; APPLICANT: Hofstadler, Steven
; APPLICANT: McNeill, John
; TITLE OF INVENTION: Molecular Interaction Sites Of Ornithine Decarboxylase
; FILE REFERENCE: IBIS0170
; CURRENT APPLICATION NUMBER: US/09/310,761
; CURRENT FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 28
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Novel Sequence
US-09-310-761-30
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Query Match      64.5%; Score 14.2; DB 17; Length 28;
Best Local Similarity 84.2%; Pred. No. 5.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Db      19 TGAGACAGATTGGGTCTC 1
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RESULT 37
US-09-310-762-30
; Sequence 30, Application US/09310762
; GENERAL INFORMATION:
; APPLICANT: Ecker, David J
; APPLICANT: Gilfeiy, Richard
; APPLICANT: Crooke, Stanley T
; APPLICANT: Sampath, Ranga
; APPLICANT: Swayze, Eric
; APPLICANT: Mohan, Venkatraman
; APPLICANT: Hofstadler, Steven
; APPLICANT: McNeill, John
; TITLE OF INVENTION: Molecular Interaction Sites Of Interleukin-4 RNA and
; FILE REFERENCE: IBIS0172
; CURRENT APPLICATION NUMBER: US/09/310,762
; CURRENT FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 28
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Novel Sequence
US-09-310-762-30
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Query Match      64.5%; Score 14.2; DB 17; Length 28;
Best Local Similarity 68.4%; Pred. No. 5.7e+03;
Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
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QY      3 GAGACCGATATCGTCTCA 21
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Db      1 GAGACCCAAAUUCUGUCUCA 19
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RESULT 38
US-09-310-762-30/C
; Sequence 30, Application US/09310762
; GENERAL INFORMATION:
; APPLICANT: Ecker, David J
; APPLICANT: Gilfeiy, Richard
; APPLICANT: Crooke, Stanley T
```

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; APPLICANT: Sampath, Ranga
; APPLICANT: Swayze, Eric
; APPLICANT: Mohan, Venkatraman
; APPLICANT: Hofstadler, Steven
; APPLICANT: McNeill, John
; TITLE OF INVENTION: Molecular Interaction Sites Of Interleukin-4 RNA and
; FILE REFERENCE: IBIS0172
; CURRENT APPLICATION NUMBER: US/09/310,762
; CURRENT FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 28
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Novel Sequence
US-09-310-762-30
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Query Match      64.5%; Score 14.2; DB 17; Length 28;
Best Local Similarity 84.2%; Pred. No. 5.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY      2 TGAGACCGATATCGTCTC 20
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Db      19 TGAGACAGATTGGGTCTC 1
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RESULT 39
US-09-310-762A-30
; Sequence 30, Application US/09310762A
; GENERAL INFORMATION:
; APPLICANT: Ecker, David J
; APPLICANT: Gilfeiy, Richard
; APPLICANT: Crooke, Stanley T
; APPLICANT: Sampath, Ranga
; APPLICANT: Swayze, Eric
; APPLICANT: Mohan, Venkatraman
; APPLICANT: Hofstadler, Steven
; APPLICANT: McNeill, John
; TITLE OF INVENTION: Molecular Interaction Sites Of Interleukin-4 RNA and
; FILE REFERENCE: IBIS0172
; CURRENT APPLICATION NUMBER: US/09/310,762A
; CURRENT FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 28
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Novel Sequence
US-09-310-762A-30
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Query Match      64.5%; Score 14.2; DB 17; Length 28;
Best Local Similarity 68.4%; Pred. No. 5.7e+03;
Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
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QY      3 GAGACCGATATCGTCTCA 21
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Db      1 GAGACCCAAAUUCUGUCUCA 19
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RESULT 40
US-09-310-762A-30/C
; Sequence 30, Application US/09310762A
; GENERAL INFORMATION:
; APPLICANT: Ecker, David J
; APPLICANT: Gilfeiy, Richard
; APPLICANT: Crooke, Stanley T
; APPLICANT: Sampath, Ranga
```

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; APPLICANT: Swayze, Eric
; APPLICANT: Mohan, Venkatarman
; APPLICANT: Hofstadler, Steven
; APPLICANT: McNeil, John
; TITLE OF INVENTION: Molecular Interaction Sites Of Interleukin-4 RNA and
; FILE REFERENCE: IBIS0172
; CURRENT APPLICATION NUMBER: US/09/310,762A
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 28
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Novel Sequence
US-09-310-762A-30

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Query Match      64.5%; Score 14.2; DB 17; Length 28;
Best Local Similarity 84.2%; Pred. No. 5.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db      19 TGAGACAGATTGGGCTC 1

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Search completed: June 14, 2003, 23:14:47
Job time : 2140 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 14, 2003, 22:15:00 ; Search time 661 Seconds
(without alignments)
229.931 Million cell updates/sec

Title: US-09-532-001-1
Perfect score: 22
Sequence: 1 CTGAGACCATATCGCTCTCAG 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7791535 seqs, 3454190175 residues

Total number of hits satisfying chosen parameters: 8630676

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 1000 summaries

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3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq.*
4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	14.8	67.3	25	US-10-355-577-403951	Sequence 403951, A
3	14.6	66.4	25	US-09-954-445A-99732	Sequence 99732, A
4	14.6	66.4	25	US-09-954-445A-99732	Sequence 99732, A
5	14.6	66.4	25	US-60-427-836-181614	Sequence 181614, A
6	14.6	66.4	25	US-60-427-836-181614	Sequence 181614, A
7	14.2	64.5	25	US-10-355-577-90477	Sequence 90477, A
8	14.2	64.5	25	US-10-355-577-90477	Sequence 90477, A
9	14	63.6	25	US-09-660-222-15526	Sequence 15526, A
10	14	63.6	25	US-09-660-222-15526	Sequence 15526, A
11	14	63.6	25	US-09-660-222-74211	Sequence 74211, A
12	14	63.6	25	US-09-660-222-74211	Sequence 74211, A
13	14	63.6	25	US-10-098-263B-30445	Sequence 30445, A
14	14	63.6	25	US-10-098-263B-30445	Sequence 30445, A
15	14	63.6	25	US-10-098-263B-30445	Sequence 30445, A
16	14	63.6	25	US-10-098-263B-70455	Sequence 70455, A
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18	14	63.6	25	US-10-098-263B-87625	Sequence 87625, A
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26	14	63.6	25	US-10-355-577-802554	Sequence 802554, A
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44	13.6	61.8	25	US-60-427-808-629395	Sequence 629395, A
45	13.4	60.9	25	US-10-355-577-548906	Sequence 548906, A
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52	13.2	60.0	25	US-10-098-263B-42695	Sequence 42695, A
53	13.2	60.0	25	US-10-355-577-31235	Sequence 31235, A
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59	13.2	60.0	25	US-10-355-577-403952	Sequence 403952, A
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66	13.2	60.0	25	US-10-355-577-697333	Sequence 697333, A
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73	13	59.1	25	US-09-660-222-15527	Sequence 15527, A
74	13	59.1	25	US-09-660-222-15527	Sequence 15527, A
75	13	59.1	25	US-09-953-570-100770	Sequence 100770, A
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77	13	59.1	25	US-09-953-570-103667	Sequence 103667, A
78	13	59.1	25	US-09-953-570-103667	Sequence 103667, A
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81	13	59.1	25	US-09-954-445A-68650	Sequence 68650, A
82	13	59.1	25	US-09-954-445A-68650	Sequence 68650, A
83	13	59.1	25	US-10-098-263B-83125	Sequence 83125, A
84	13	59.1	25	US-10-098-263B-83125	Sequence 83125, A
85	13	59.1	25	US-10-098-263B-83125	Sequence 83125, A
86	13	59.1	25	US-10-355-577-305911	Sequence 305911, A
87	13	59.1	25	US-10-355-577-305911	Sequence 305911, A
88	13	59.1	25	US-10-355-577-371036	Sequence 371036, A
89	13	59.1	25	US-10-355-577-371036	Sequence 371036, A
90	13	59.1	25	US-10-355-577-402225	Sequence 402225, A
91	13	59.1	25	US-10-355-577-402225	Sequence 402225, A
92	13	59.1	25	US-10-355-577-519794	Sequence 519794, A
93	13	59.1	25	US-10-355-577-519794	Sequence 519794, A
94	13	59.1	25	US-10-355-577-631872	Sequence 631872, A
95	13	59.1	25	US-10-355-577-631872	Sequence 631872, A

C 96	13	59.1	25	9	US-10-355-577-797529	Sequence 797529,	169	12.8	58.2	25	11	US-60-427-808-905653	Sequence 905653,
C 97	13	59.1	25	9	US-10-355-577-875225	Sequence 875225,	C 170	12.8	58.2	25	11	US-60-427-808-905653	Sequence 905653,
C 98	13	59.1	25	9	US-10-355-577-875225	Sequence 875225,	C 171	12.6	57.3	25	5	US-09-660-080B-1605	Sequence 1605,
C 99	13	59.1	25	10	US-60-469-545-35396	Sequence 35396,	C 172	12.6	57.3	25	5	US-09-660-080B-1605	Sequence 1605,
C 100	13	59.1	25	10	US-60-469-545-35396	Sequence 35396,	C 173	12.6	57.3	25	5	US-09-660-080B-1605	Sequence 1605,
C 101	13	59.1	25	10	US-60-469-545-35886	Sequence 35886,	C 174	12.6	57.3	25	5	US-09-660-080B-1605	Sequence 1605,
C 102	13	59.1	25	10	US-60-469-545-35886	Sequence 35886,	C 175	12.6	57.3	25	6	US-09-660-222-85019	Sequence 85019,
C 103	13	59.1	25	10	US-60-469-545-202291	Sequence 202291,	C 176	12.6	57.3	25	6	US-09-660-222-85019	Sequence 85019,
C 104	13	59.1	25	10	US-60-469-545-202291	Sequence 202291,	C 177	12.6	57.3	25	7	US-09-954-445A-33743	Sequence 33743,
C 105	13	59.1	25	10	US-60-469-545-202781	Sequence 202781,	C 178	12.6	57.3	25	7	US-09-954-445A-33743	Sequence 33743,
C 106	13	59.1	25	10	US-60-469-545-202781	Sequence 202781,	C 179	12.6	57.3	25	7	US-09-954-445A-33744	Sequence 33744,
C 107	13	59.1	25	11	US-60-427-808-380944	Sequence 380944,	C 180	12.6	57.3	25	7	US-09-954-445A-33744	Sequence 33744,
C 108	13	59.1	25	11	US-60-427-808-380944	Sequence 380944,	C 181	12.6	57.3	25	7	US-09-954-445A-99983	Sequence 99983,
C 109	13	59.1	25	11	US-60-427-808-509558	Sequence 509558,	C 182	12.6	57.3	25	7	US-09-954-445A-99983	Sequence 99983,
C 110	13	59.1	25	11	US-60-427-808-509558	Sequence 509558,	C 183	12.6	57.3	25	7	US-09-954-445A-128650	Sequence 128650,
C 111	13	59.1	25	11	US-60-427-808-689447	Sequence 689447,	C 184	12.6	57.3	25	7	US-09-954-445A-128650	Sequence 128650,
C 112	13	59.1	25	11	US-60-427-808-689447	Sequence 689447,	C 185	12.6	57.3	25	7	US-09-954-445A-128651	Sequence 128651,
C 113	13	59.1	25	11	US-60-427-808-734492	Sequence 734492,	C 186	12.6	57.3	25	7	US-09-954-445A-128651	Sequence 128651,
C 114	13	59.1	25	11	US-60-427-808-734492	Sequence 734492,	C 187	12.6	57.3	25	9	US-10-098-263B-13073	Sequence 13073,
C 115	13	59.1	25	11	US-60-427-808-851327	Sequence 851327,	C 188	12.6	57.3	25	9	US-10-098-263B-13073	Sequence 13073,
C 116	13	59.1	25	11	US-60-427-808-851327	Sequence 851327,	C 189	12.6	57.3	25	9	US-10-355-577-55941	Sequence 55941,
C 117	13	59.1	25	11	US-60-427-836-82442	Sequence 82442,	C 190	12.6	57.3	25	9	US-10-355-577-55941	Sequence 55941,
C 118	13	59.1	25	11	US-60-427-836-82442	Sequence 82442,	C 191	12.6	57.3	25	9	US-10-355-577-55942	Sequence 55942,
C 119	13	59.1	25	11	US-60-427-836-181612	Sequence 181612,	C 192	12.6	57.3	25	9	US-10-355-577-55942	Sequence 55942,
C 120	13	59.1	25	11	US-60-427-836-181612	Sequence 181612,	C 193	12.6	57.3	25	9	US-10-355-577-90478	Sequence 90478,
C 121	13	59.1	25	11	US-60-427-836-322172	Sequence 322172,	C 194	12.6	57.3	25	9	US-10-355-577-90478	Sequence 90478,
C 122	13	59.1	25	11	US-60-427-836-322172	Sequence 322172,	C 195	12.6	57.3	25	9	US-10-355-577-283495	Sequence 283495,
C 123	13	59.1	25	11	US-60-427-836-322173	Sequence 322173,	C 196	12.6	57.3	25	9	US-10-355-577-283495	Sequence 283495,
C 124	13	59.1	25	11	US-60-427-836-322173	Sequence 322173,	C 197	12.6	57.3	25	9	US-10-355-577-297457	Sequence 297457,
C 125	13	59.1	25	11	US-60-427-836-625110	Sequence 625110,	C 198	12.6	57.3	25	9	US-10-355-577-297457	Sequence 297457,
C 126	13	59.1	25	11	US-60-427-836-625110	Sequence 625110,	C 199	12.6	57.3	25	9	US-10-355-577-337874	Sequence 337874,
C 127	13	59.1	25	11	US-60-427-836-625110	Sequence 625110,	C 200	12.6	57.3	25	9	US-10-355-577-337874	Sequence 337874,
C 128	13	59.1	25	11	US-60-427-836-648567	Sequence 648567,	C 201	12.6	57.3	25	9	US-10-355-577-540297	Sequence 540297,
C 129	13	59.1	36	6	US-09-551-151A-49	Sequence 49,	C 202	12.6	57.3	25	9	US-10-355-577-540297	Sequence 540297,
C 130	13	59.1	36	6	US-09-551-151A-49	Sequence 49,	C 203	12.6	57.3	25	9	US-10-355-577-564953	Sequence 564953,
C 131	13	59.1	24	6	US-09-084-303B-45	Sequence 45,	C 204	12.6	57.3	25	9	US-10-355-577-564953	Sequence 564953,
C 132	13	59.1	24	6	US-09-084-303B-45	Sequence 45,	C 205	12.6	57.3	25	9	US-10-355-577-639291	Sequence 639291,
C 133	13	59.1	24	9	US-10-339-740-45	Sequence 45,	C 206	12.6	57.3	25	9	US-10-355-577-639291	Sequence 639291,
C 134	13	59.1	24	9	US-10-339-740-45	Sequence 45,	C 207	12.6	57.3	25	9	US-10-355-577-735589	Sequence 735589,
C 135	13	59.1	25	5	US-09-660-080B-14713	Sequence 14713,	C 208	12.6	57.3	25	9	US-10-355-577-735589	Sequence 735589,
C 136	13	59.1	25	5	US-09-660-080B-14713	Sequence 14713,	C 209	12.6	57.3	25	9	US-10-355-577-887212	Sequence 887212,
C 137	13	59.1	25	5	US-09-660-080B-14714	Sequence 14714,	C 210	12.6	57.3	25	9	US-10-355-577-887212	Sequence 887212,
C 138	13	59.1	25	5	US-09-660-080B-14714	Sequence 14714,	C 211	12.6	57.3	25	9	US-10-355-577-898442	Sequence 898442,
C 139	13	59.1	25	6	US-09-660-222-93360	Sequence 93360,	C 212	12.6	57.3	25	9	US-10-355-577-898442	Sequence 898442,
C 140	13	59.1	25	6	US-09-660-222-93360	Sequence 93360,	C 213	12.6	57.3	25	9	US-10-355-577-899706	Sequence 899706,
C 141	13	59.1	25	7	US-09-954-445A-119613	Sequence 119613,	C 214	12.6	57.3	25	9	US-10-355-577-899706	Sequence 899706,
C 142	13	59.1	25	7	US-09-954-445A-119613	Sequence 119613,	C 215	12.6	57.3	25	11	US-60-427-808-5895	Sequence 5895,
C 143	13	59.1	25	7	US-09-954-445A-130471	Sequence 130471,	C 216	12.6	57.3	25	11	US-60-427-808-5895	Sequence 5895,
C 144	13	59.1	25	7	US-09-954-445A-130471	Sequence 130471,	C 217	12.6	57.3	25	11	US-60-427-808-145394	Sequence 145394,
C 145	13	59.1	25	9	US-10-098-263B-60005	Sequence 60005,	C 218	12.6	57.3	25	11	US-60-427-808-145394	Sequence 145394,
C 146	13	59.1	25	9	US-10-098-263B-60005	Sequence 60005,	C 219	12.6	57.3	25	11	US-60-427-808-150969	Sequence 150969,
C 147	13	59.1	25	9	US-10-098-263B-88139	Sequence 88139,	C 220	12.6	57.3	25	11	US-60-427-808-150969	Sequence 150969,
C 148	13	59.1	25	9	US-10-098-263B-88139	Sequence 88139,	C 221	12.6	57.3	25	11	US-60-427-808-150969	Sequence 150969,
C 149	13	59.1	25	9	US-10-355-577-75051	Sequence 75051,	C 222	12.6	57.3	25	11	US-60-427-808-158974	Sequence 158974,
C 150	13	59.1	25	9	US-10-355-577-75051	Sequence 75051,	C 223	12.6	57.3	25	11	US-60-427-808-158974	Sequence 158974,
C 151	13	59.1	25	9	US-10-355-577-509664	Sequence 509664,	C 224	12.6	57.3	25	11	US-60-427-808-194934	Sequence 194934,
C 152	13	59.1	25	9	US-10-355-577-509664	Sequence 509664,	C 225	12.6	57.3	25	11	US-60-427-808-194934	Sequence 194934,
C 153	13	59.1	25	9	US-10-355-577-788258	Sequence 788258,	C 226	12.6	57.3	25	11	US-60-427-808-368723	Sequence 368723,
C 154	13	59.1	25	9	US-10-355-577-788258	Sequence 788258,	C 227	12.6	57.3	25	11	US-60-427-808-368723	Sequence 368723,
C 155	13	59.1	25	9	US-10-355-577-940701	Sequence 940701,	C 228	12.6	57.3	25	11	US-60-427-808-421708	Sequence 421708,
C 156	13	59.1	25	9	US-10-355-577-940701	Sequence 940701,	C 229	12.6	57.3	25	11	US-60-427-808-421708	Sequence 421708,
C 157	13	59.1	25	10	US-60-469-545-74158	Sequence 74158,	C 230	12.6	57.3	25	11	US-60-427-808-630651	Sequence 630651,
C 158	13	59.1	25	10	US-60-469-545-74158	Sequence 74158,	C 231	12.6	57.3	25	11	US-60-427-808-630651	Sequence 630651,
C 159	13	59.1	25	10	US-60-469-545-74643	Sequence 74643,	C 232	12.6	57.3	25	11	US-60-427-808-660744	Sequence 660744,
C 160	13	59.1	25	10	US-60-469-545-74643	Sequence 74643,	C 233	12.6	57.3	25	11	US-60-427-808-660745	Sequence 660745,
C 161	13	59.1	25	10	US-60-469-545-163534	Sequence 163534,	C 234	12.6	57.3	25	11	US-60-427-808-660745	Sequence 660745,
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C 163	13	59.1	25	10	US-60-469-545-164019	Sequence 164019,	C 236	12.6	57.3	25	11	US-60-427-808-669784	Sequence 669784,
C 164	13	59.1	25	10	US-60-469-545-164019	Sequence 164019,	C 237	12.6	57.3	25	11	US-60-427-808-698831	Sequence 698831,
C 165	13	59.1	25	11	US-60-427-808-511584	Sequence 511584,	C 238	12.6	57.3	25	11	US-60-427-808-698831	Sequence 698831,
C 166	13	59.1	25	11	US-60-427-808-511584	Sequence 511584,	C 239	12.6	57.3	25	11	US-60-427-808-811370	Sequence 811370,
C 167	13	59.1	25	11	US-60-427-808-581182	Sequence 581182,	C 240	12.6	57.3	25	11	US-60-427-808-811370	Sequence 811370,
C 168	13	59.1	25	11	US-60-427-808-581182	Sequence 581182,	C 241	12.6	57.3	25	11	US-60-427-808-820239	Sequence 820239,

C 242	12.6	57.3	25	11	US-60-427-808-820299	Sequence 820299, A	315	12.4	56.4	25	9	US-10-355-577-579566	Sequence 579566, A
C 243	12.6	57.3	25	11	US-60-427-836-48799	Sequence 48799, A	316	12.4	56.4	25	9	US-10-355-577-579566	Sequence 579566, A
C 244	12.6	57.3	25	11	US-60-427-836-48799	Sequence 48799, A	317	12.4	56.4	25	9	US-10-355-577-608149	Sequence 608149, A
C 245	12.6	57.3	25	11	US-60-427-836-387512	Sequence 387512, A	318	12.4	56.4	25	9	US-10-355-577-608149	Sequence 608149, A
C 246	12.6	57.3	25	11	US-60-427-836-387512	Sequence 387512, A	319	12.4	56.4	25	9	US-10-355-577-626708	Sequence 626708, A
C 247	12.6	57.3	25	11	US-60-427-836-482669	Sequence 482669, A	320	12.4	56.4	25	9	US-10-355-577-626708	Sequence 626708, A
C 248	12.6	57.3	25	11	US-60-427-836-482669	Sequence 482669, A	321	12.4	56.4	25	9	US-10-355-577-802553	Sequence 802553, A
C 249	12.6	57.3	25	11	US-60-427-836-504798	Sequence 504798, A	322	12.4	56.4	25	9	US-10-355-577-802553	Sequence 802553, A
C 250	12.6	57.3	25	11	US-60-427-836-504798	Sequence 504798, A	323	12.4	56.4	25	9	US-10-355-577-814469	Sequence 814469, A
C 251	12.6	57.3	25	11	US-60-427-836-504798	Sequence 504798, A	324	12.4	56.4	25	9	US-10-355-577-814469	Sequence 814469, A
C 252	12.6	57.3	25	11	US-60-427-836-504798	Sequence 504798, A	325	12.4	56.4	25	9	US-10-355-577-814470	Sequence 814470, A
C 253	12.6	57.3	50	1	PCT-US03-13015-879	Sequence 879, App	326	12.4	56.4	25	9	US-10-355-577-814470	Sequence 814470, A
C 254	12.6	57.3	50	1	PCT-US03-13015-879	Sequence 879, App	327	12.4	56.4	25	9	US-10-355-577-825522	Sequence 825522, A
C 255	12.6	57.3	50	9	US-10-325-899-2060	Sequence 2060, Ap	328	12.4	56.4	25	9	US-10-355-577-825522	Sequence 825522, A
C 256	12.6	57.3	50	9	US-10-325-899-2060	Sequence 2060, Ap	329	12.4	56.4	25	9	US-10-355-577-923571	Sequence 923571, A
C 257	12.4	56.4	21	9	US-10-035-9788A-33	Sequence 33, Appl	330	12.4	56.4	25	9	US-10-355-577-923571	Sequence 923571, A
C 258	12.4	56.4	21	9	US-10-035-9788A-33	Sequence 33, Appl	331	12.4	56.4	25	9	US-10-355-577-954030	Sequence 954030, A
C 259	12.4	56.4	25	5	US-09-660-080B-10372	Sequence 10272, A	332	12.4	56.4	25	9	US-10-355-577-954030	Sequence 954030, A
C 260	12.4	56.4	25	5	US-09-660-080B-10372	Sequence 10272, A	333	12.4	56.4	25	10	US-60-470-475-93594	Sequence 93594, A
C 261	12.4	56.4	25	6	US-09-660-222-62449	Sequence 62449, A	334	12.4	56.4	25	10	US-60-470-475-93594	Sequence 93594, A
C 262	12.4	56.4	25	6	US-09-660-222-62449	Sequence 62449, A	335	12.4	56.4	25	10	US-60-470-475-100402	Sequence 100402, A
C 263	12.4	56.4	25	6	US-09-660-222-62449	Sequence 62449, A	336	12.4	56.4	25	10	US-60-470-475-100402	Sequence 100402, A
C 264	12.4	56.4	25	6	US-09-660-222-62449	Sequence 62449, A	337	12.4	56.4	25	11	US-60-417-190-16466	Sequence 16466, A
C 265	12.4	56.4	25	6	US-09-660-222-114462	Sequence 114462, A	338	12.4	56.4	25	11	US-60-417-190-16466	Sequence 16466, A
C 266	12.4	56.4	25	6	US-09-660-222-114462	Sequence 114462, A	339	12.4	56.4	25	11	US-60-417-190-18551	Sequence 18551, A
C 267	12.4	56.4	25	6	US-09-660-222-114463	Sequence 114463, A	340	12.4	56.4	25	11	US-60-417-190-18551	Sequence 18551, A
C 268	12.4	56.4	25	6	US-09-660-222-114463	Sequence 114463, A	341	12.4	56.4	25	11	US-60-427-808-296571	Sequence 296571, A
C 269	12.4	56.4	25	6	US-09-660-222-139083	Sequence 139083, A	342	12.4	56.4	25	11	US-60-427-808-296571	Sequence 296571, A
C 270	12.4	56.4	25	6	US-09-660-222-139083	Sequence 139083, A	343	12.4	56.4	25	11	US-60-427-808-313509	Sequence 313509, A
C 271	12.4	56.4	25	7	US-09-953-570-137844	Sequence 137844, A	344	12.4	56.4	25	11	US-60-427-808-313509	Sequence 313509, A
C 272	12.4	56.4	25	7	US-09-953-570-137844	Sequence 137844, A	345	12.4	56.4	25	11	US-60-427-808-380946	Sequence 380946, A
C 273	12.4	56.4	25	7	US-09-954-445A-11503	Sequence 11503, A	346	12.4	56.4	25	11	US-60-427-808-380946	Sequence 380946, A
C 274	12.4	56.4	25	7	US-09-954-445A-11503	Sequence 11503, A	347	12.4	56.4	25	11	US-60-427-808-389384	Sequence 389384, A
C 275	12.4	56.4	25	9	US-10-098-263B-21859	Sequence 21859, A	348	12.4	56.4	25	11	US-60-427-808-389384	Sequence 389384, A
C 276	12.4	56.4	25	9	US-10-098-263B-21859	Sequence 21859, A	349	12.4	56.4	25	11	US-60-427-808-734095	Sequence 734095, A
C 277	12.4	56.4	25	9	US-10-098-263B-30446	Sequence 30446, A	350	12.4	56.4	25	11	US-60-427-808-734095	Sequence 734095, A
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C 279	12.4	56.4	25	9	US-10-098-263B-70456	Sequence 70456, A	352	12.4	56.4	25	11	US-60-427-808-811514	Sequence 811514, A
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C 281	12.4	56.4	25	9	US-10-098-263B-87626	Sequence 87626, A	354	12.4	56.4	25	11	US-60-427-808-832054	Sequence 832054, A
C 282	12.4	56.4	25	9	US-10-098-263B-87626	Sequence 87626, A	355	12.4	56.4	25	11	US-60-427-808-832292	Sequence 832292, A
C 283	12.4	56.4	25	9	US-10-098-263B-99206	Sequence 99206, A	356	12.4	56.4	25	11	US-60-427-808-832292	Sequence 832292, A
C 284	12.4	56.4	25	9	US-10-098-263B-99206	Sequence 99206, A	357	12.4	56.4	25	11	US-60-427-836-85201	Sequence 85201, A
C 285	12.4	56.4	25	9	US-10-098-263B-105386	Sequence 105386, A	358	12.4	56.4	25	11	US-60-427-836-85201	Sequence 85201, A
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C 287	12.4	56.4	25	9	US-10-355-577-84972	Sequence 84972, A	360	12.4	56.4	25	11	US-60-427-836-126554	Sequence 126554, A
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C 289	12.4	56.4	25	9	US-10-355-577-167123	Sequence 167123, A	362	12.4	56.4	25	11	US-60-427-836-194481	Sequence 194481, A
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C 291	12.4	56.4	25	9	US-10-355-577-194918	Sequence 194918, A	364	12.4	56.4	25	11	US-60-427-836-218811	Sequence 218811, A
C 292	12.4	56.4	25	9	US-10-355-577-194918	Sequence 194918, A	365	12.4	56.4	25	11	US-60-427-836-218811	Sequence 218811, A
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C 297	12.4	56.4	25	9	US-10-355-577-387487	Sequence 387487, A	370	12.2	55.5	20	9	US-10-310-188-36880	Sequence 36880, A
C 298	12.4	56.4	25	9	US-10-355-577-387487	Sequence 387487, A	371	12.2	55.5	25	6	US-09-660-222-331414	Sequence 331414, A
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C 301	12.4	56.4	25	9	US-10-355-577-440638	Sequence 440638, A	374	12.2	55.5	25	6	US-09-660-222-81573	Sequence 81573, A
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ALIGNMENTS

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; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 403951
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
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Db 2 GAGACCGATATCGGTCTC 19

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; Sequence 403951, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 403951
; LENGTH: 25
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; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-403951
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Best Local Similarity 88.9%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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; Sequence 99732, Application US/09954445A
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Arabidopsis Thaliana
; FILE REFERENCE: 3116.1
; CURRENT APPLICATION NUMBER: US/09/954,445A
; CURRENT FILING DATE: 2000-09-17
; PRIOR APPLICATION NUMBER: 60/233,620
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 131820
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
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; ORGANISM: Arabidopsis thaliana
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; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Arabidopsis Thaliana
; FILE REFERENCE: 3116.1
; CURRENT APPLICATION NUMBER: US/09/954,445A
; CURRENT FILING DATE: 2000-09-17
; PRIOR APPLICATION NUMBER: 60/233,620
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 131820
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 99732
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; ORGANISM: Arabidopsis thaliana
US-09-954-445A-99732
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Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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RESULT 5
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; GENERAL INFORMATION:
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; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
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; CURRENT APPLICATION NUMBER: US/60/427,836
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
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```

```
QY 1 CTGAGACCGATATCGTCTCA 21
    |||||
Db 5 CTGAGACCGATATCGAGGCA 25
```

```
RESULT 6
US-60-427-836-181614/c
; Sequence 181614, Application US/60427836
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527
; CURRENT APPLICATION NUMBER: US/60/427,836
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 181614
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-60-427-836-181614
```

```
Query Match          66.4%; Score 14.6; DB 11; Length 25;
Best Local Similarity 81.0%; Pred. No. 1.8e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 2 TGAGACCGATATCGTCTCAG 22
    |||||
Db 25 TGCCTCCATATCGTCTCAG 5
```

```
RESULT 7
US-10-355-577-90477
; Sequence 90477, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 90477
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-90477
```

```
Query Match          64.5%; Score 14.2; DB 9; Length 25;
Best Local Similarity 84.2%; Pred. No. 2.9e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 3 GAGACCGATATCGTCTCA 21
    |||||
Db 6 GAGACCGATATCGGTATGA 24
```

```
RESULT 8
US-10-355-577-90477/c
; Sequence 90477, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 90477
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-90477
```

```
Query Match          64.5%; Score 14.2; DB 9; Length 25;
Best Local Similarity 84.2%; Pred. No. 2.9e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 2 TGAGACCGATATCGTCTC 20
    |||||
Db 24 TCATACCGATATCGTCTC 6
```

```
RESULT 9
US-09-660-222-15526
; Sequence 15526, Application US/09660222
; GENERAL INFORMATION:
; APPLICANT: Miltmann et al.
; TITLE OF INVENTION: Methods of Genetic Analysis of Human
; FILE REFERENCE: 3102.1
; CURRENT APPLICATION NUMBER: US/09/660,222
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/164,973
; PRIOR FILING DATE: 1999-11-11
; NUMBER OF SEQ ID NOS: 140981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15526
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank D87073
US-09-660-222-15526
```

```
Query Match          63.6%; Score 14; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 9 GATATCGTCTCAG 22
    |||||
Db 1 GATATCGTCTCAG 14
```

```
RESULT 10
US-09-660-222-15526/c
; Sequence 15526, Application US/09660222
; GENERAL INFORMATION:
; APPLICANT: Miltmann et al.
; TITLE OF INVENTION: Methods of Genetic Analysis of Human
; FILE REFERENCE: 3102.1
; CURRENT APPLICATION NUMBER: US/09/660,222
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/164,973
; PRIOR FILING DATE: 1999-11-11
; NUMBER OF SEQ ID NOS: 140981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15526
```

```
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank D87073
US-09-660-222-15526

Query Match          63.6%; Score 14; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CTGAGACCGATATC 14
Db 14 CTGAGACCGATATC 1

RESULT 11
US-09-660-222-74211
; Sequence 74211, Application US/09660222
; GENERAL INFORMATION:
; APPLICANT: Miltmann et al.
; TITLE OF INVENTION: Methods of Genetic Analysis of Human
; FILE REFERENCE: 3102.1
; CURRENT APPLICATION NUMBER: US/09/660,222
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/164,973
; PRIOR FILING DATE: 1999-11-11
; NUMBER OF SEQ ID NOS: 140981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 74211
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank U00951
US-09-660-222-74211

Query Match          63.6%; Score 14; DB 6; Length 25;
Best Local Similarity 77.3%; Pred. No. 3.6e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 1 CTGAGACCGATATCGTCTCAG 22
Db 2 CTGATACCAATATGATGCTCCG 23

RESULT 12
US-09-660-222-74211/c
; Sequence 74211, Application US/09660222
; GENERAL INFORMATION:
; APPLICANT: Miltmann et al.
; TITLE OF INVENTION: Methods of Genetic Analysis of Human
; FILE REFERENCE: 3102.1
; CURRENT APPLICATION NUMBER: US/09/660,222
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/164,973
; PRIOR FILING DATE: 1999-11-11
; NUMBER OF SEQ ID NOS: 140981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 74211
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank U00951
US-09-660-222-74211

Query Match          63.6%; Score 14; DB 6; Length 25;
Best Local Similarity 77.3%; Pred. No. 3.6e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 1 CTGAGACCGATATCGTCTCAG 22
Db 2 CTGATACCAATATGATGCTCCG 23

RESULT 13
US-10-098-263B-30445
; Sequence 30445, Application US/10098263B
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 30445
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-30445

Query Match          63.6%; Score 14; DB 9; Length 25;
Best Local Similarity 77.3%; Pred. No. 3.6e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 1 CTGAGACCGATATCGTCTCAG 22
Db 3 CTCTACCGATATTTGCTCAG 24

RESULT 14
US-10-098-263B-30445/c
; Sequence 30445, Application US/10098263B
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 30445
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-30445

Query Match          63.6%; Score 14; DB 9; Length 25;
Best Local Similarity 77.3%; Pred. No. 3.6e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 1 CTGAGACCGATATCGTCTCAG 22
Db 24 CTGAGACCAATATCGTAGAG 3

RESULT 15
US-10-098-263B-70455
; Sequence 70455, Application US/10098263B
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
```

```
Oy 1 CTGAGACCGATATCGTCTCAG 22
Db 23 CGGAGACTCATATTGCTATCAG 2

RESULT 13
US-10-098-263B-30445
; Sequence 30445, Application US/10098263B
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 30445
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-30445

Query Match          63.6%; Score 14; DB 9; Length 25;
Best Local Similarity 77.3%; Pred. No. 3.6e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 1 CTGAGACCGATATCGTCTCAG 22
Db 3 CTCTACCGATATTTGCTCAG 24

RESULT 14
US-10-098-263B-30445/c
; Sequence 30445, Application US/10098263B
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 30445
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-30445

Query Match          63.6%; Score 14; DB 9; Length 25;
Best Local Similarity 77.3%; Pred. No. 3.6e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 1 CTGAGACCGATATCGTCTCAG 22
Db 24 CTGAGACCAATATCGTAGAG 3

RESULT 15
US-10-098-263B-70455
; Sequence 70455, Application US/10098263B
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
```

```
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 70455
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-70455
```

```
Query Match          63.6%; Score 14; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 9 GATATCGGTCTCAG 22
    |||||
Db 5 GATATCGGTCTCAG 18
```

```
RESULT 16
US-10-098-263B-70455/c
; Sequence 70455, Application US/10098263B
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 70455
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-70455
```

```
Query Match          63.6%; Score 14; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 CTGAGACCGATATC 14
    |||||
Db 18 CTGAGACCGATATC 5
```

```
RESULT 17
US-10-098-263B-87625
; Sequence 87625, Application US/10098263B
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 87625
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-87625
```

```
Query Match          63.6%; Score 14; DB 9; Length 25;
Best Local Similarity 77.3%; Pred. No. 3.6e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
QY 1 CTGAGACCGATATCGTCTCAG 22
    |||||
Db 2 CTGATACCATATGAGTCTCCG 23
```

RESULT 18

```
US-10-098-263B-87625/c
; Sequence 87625, Application US/10098263B
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 87625
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-87625
```

```
Query Match          63.6%; Score 14; DB 9; Length 25;
Best Local Similarity 77.3%; Pred. No. 3.6e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
QY 1 CTGAGACCGATATCGTCTCAG 22
    |||||
Db 23 CCGAGACTCATATGCGTATCAG 2
```

```
RESULT 19
US-10-098-263B-105385
; Sequence 105385, Application US/10098263B
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 105385
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-105385
```

```
Query Match          63.6%; Score 14; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 9 GATATCGGTCTCAG 22
    |||||
Db 1 GATATCGGTCTCAG 14
```

```
RESULT 20
US-10-098-263B-105385/c
; Sequence 105385, Application US/10098263B
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 105385
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-105385
```

Query Match 63.6%; Score 14; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGAGACCGATATC 14
DB 14 CTGAGACCGATATC 1

RESULT 21
US-10-355-577-316225
; Sequence 316225, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 316225
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-316225

Query Match 63.6%; Score 14; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GATATCGTCTCAG 22
DB 4 GATATCGTCTCAG 17

RESULT 22
US-10-355-577-316225/C
; Sequence 316225, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 316225
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-316225

Query Match 63.6%; Score 14; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGAGACCGATATC 14
DB 17 CTGAGACCGATATC 4

RESULT 23
US-10-355-577-576645
; Sequence 576645, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 576645
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-576645

Query Match 63.6%; Score 14; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GATATCGTCTCAG 22
DB 1 GATATCGTCTCAG 14

RESULT 24
US-10-355-577-576645/C
; Sequence 576645, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 576645
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-576645

Query Match 63.6%; Score 14; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGAGACCGATATC 14
DB 14 CTGAGACCGATATC 1

RESULT 25
US-10-355-577-802554
; Sequence 802554, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 802554
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-802554

Query Match 63.6%; Score 14; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GATATCGTCTCAG 22
DB 5 GATATCGTCTCAG 18

RESULT 26
US-10-355-577-802554/C
; Sequence 802554, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133

```
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 802554
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-802554
```

```
Query Match 63.6%; Score 14; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 CTGAGACCGATATC 14
Db 18 CTGAGACCGATATC 5
```

```
RESULT 27
US-10-355-577-320105
; Sequence 320105, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 320105
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-320105
```

```
Query Match 62.7%; Score 13.8; DB 9; Length 25;
Best Local Similarity 88.2%; Pred. No. 4.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 5 GACCGATATCGGCTCA 21
Db 8 GACGATATCGATCTCA 24
```

```
RESULT 28
US-10-355-577-320105/c
; Sequence 320105, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 320105
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-320105
```

```
Query Match 62.7%; Score 13.8; DB 9; Length 25;
Best Local Similarity 88.2%; Pred. No. 4.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 2 TGAGACCGATATCGTC 18
Db 24 TGAGATGATATCTGTC 8
```

RESULT 29

```
US-10-355-577-559692
; Sequence 559692, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 559692
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-559692
```

```
Query Match 62.7%; Score 13.8; DB 9; Length 25;
Best Local Similarity 88.2%; Pred. No. 4.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 3 GAGACCGATATCGGTC 19
Db 1 GAGACCGAATCGTCT 17
```

```
RESULT 30
US-10-355-577-559692/c
; Sequence 559692, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 559692
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-559692
```

```
Query Match 62.7%; Score 13.8; DB 9; Length 25;
Best Local Similarity 88.2%; Pred. No. 4.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 4 AGACCGATATCGGTC 20
Db 17 AGAACGATTCGGCTTC 1
```

```
RESULT 31
US-09-954-445A-48359
; Sequence 48359, Application US/0995445A
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Arabidopsis Thaliana
; FILE REFERENCE: 3116.1
; CURRENT APPLICATION NUMBER: US/09/954,445A
; CURRENT FILING DATE: 2000-09-17
; PRIOR APPLICATION NUMBER: 60/233,620
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 131820
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 48359
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-954-445A-48359
```

```
Query Match 61.8%; Score 13.6; DB 7; Length 25;
Best Local Similarity 80.0%; Pred. No. 5.8e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

OY 2 TGAGACCGATATCGGTCTCA 21
Db 2 TCAGACGATATTCGTCTGCA 21

RESULT 32
US-09-954-445A-48359/C
; Sequence 48359, Application US/09954445A
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Arabidopsis Thaliana
; FILE REFERENCE: 3116.1
; CURRENT APPLICATION NUMBER: US/09/954,445A
; CURRENT FILING DATE: 2000-09-17
; PRIOR APPLICATION NUMBER: 60/233,620
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 131820
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 48359
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-954-445A-48359

Query Match 61.8%; Score 13.6; DB 7; Length 25;
Best Local Similarity 80.0%; Pred. No. 5.8e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 TGAGACCGATATCGGTCTCA 21
Db 21 TCGACCGCATATACGTCTGA 2

RESULT 33
US-10-098-263B-67902
; Sequence 67902, Application US/10098263B
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 67902
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-67902

Query Match 61.8%; Score 13.6; DB 9; Length 25;
Best Local Similarity 80.0%; Pred. No. 5.8e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 CTGAGACCGATATCGGTCTC 20
Db 4 CGGAGACAGATTTCGGTCCG 23

RESULT 34
US-10-098-263B-67902/C
; Sequence 67902, Application US/10098263B
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16

; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 67902
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-67902

Query Match 61.8%; Score 13.6; DB 9; Length 25;
Best Local Similarity 80.0%; Pred. No. 5.8e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 3 GAGACCGATATCGGTCTCAG 22
Db 23 GCGACCGAATTCGTCTCCG 4

RESULT 35
US-10-098-263B-93368
; Sequence 93368, Application US/10098263B
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 93368
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-93368

Query Match 61.8%; Score 13.6; DB 9; Length 25;
Best Local Similarity 80.0%; Pred. No. 5.8e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 CTGAGACCGATATCGGTCTC 20
Db 2 CGGAGACAGATTTCGGTCCG 21

RESULT 36
US-10-098-263B-93368/C
; Sequence 93368, Application US/10098263B
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 93368
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-93368

Query Match 61.8%; Score 13.6; DB 9; Length 25;
Best Local Similarity 80.0%; Pred. No. 5.8e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 3 GAGACCGATATCGGTCTCAG 22
Db 21 GCGACCGAATTCGTCTCCG 2


```

RESULT 37
US-10-355-577-404087
; Sequence 404087, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 404087
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-404087

Query Match      61.8%; Score 13.6; DB 9; Length 25;
Best Local Similarity 80.0%; Pred. No. 5.8e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      3 GAGACCGATATCGGTCTCAG 22
Db      2 GAGACCGATATCGGTCTCAG 21

RESULT 38
US-10-355-577-404087/C
; Sequence 404087, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 404087
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-404087

Query Match      61.8%; Score 13.6; DB 9; Length 25;
Best Local Similarity 80.0%; Pred. No. 5.8e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 CTGAGACCGATATCGGTCTC 20
Db      21 CCGAGTCCGGTATCCGTCTC 2

RESULT 39
US-10-355-577-700753
; Sequence 700753, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 700753
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-700753

Query Match      61.8%; Score 13.6; DB 9; Length 25;
Best Local Similarity 80.0%; Pred. No. 5.8e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 CTGAGACCGATATCGGTCTC 20
Db      21 CCGAGTCCGGTATCCGTCTC 2

Query Match      61.8%; Score 13.6; DB 9; Length 25;
Best Local Similarity 80.0%; Pred. No. 5.8e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

```

QY      3 GAGACCGATATCGGTCTCAG 22
Db      4 GATACCTTATAGTCTCAG 23

RESULT 40
US-10-355-577-700753/C
; Sequence 700753, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 700753
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-700753

Query Match      61.8%; Score 13.6; DB 9; Length 25;
Best Local Similarity 80.0%; Pred. No. 5.8e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 CTGAGACCGATATCGGTCTC 20
Db      23 CTGAGACCTTATAGGTATC 4

```

Search completed: June 14, 2003, 23:26:57
Job time : 667 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 14, 2003, 09:51:10 ; Search time 979 Seconds
(without alignments)
653.996 Million cell updates/sec

Title: US-09-532-001-1

Perfect score: 22

Sequence: 1 CTGAGACCGATATCGGTCTCAG 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 841850

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 1000 summaries

Database :

GeneBld: *
1: gb_ba: *
2: gb_hcg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
14: gb_vl: *
15: em_ba: *
16: em_fun: *
17: em_hum: *
18: em_in: *
19: em_mu: *
20: em_om: *
21: em_or: *
22: em_ov: *
23: em_pat: *
24: em_ph: *
25: em_pl: *
26: em_ro: *
27: em_sts: *
28: em_un: *
29: em_vl: *
30: em_hcg_hum: *
31: em_hcg_inv: *
32: em_hcg_other: *
33: em_hcg_mus: *
34: em_hcg_pln: *
35: em_hcg_rtd: *
36: em_hcg_man: *
37: em_hcg_vtl: *
38: em_sy: *
39: em_hlgo_hum: *
40: em_hlgo_mus: *
41: em_hlgo_other: *

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	13.4	60.9	20	6 AX295560	AX295560 Sequence
2	13.4	60.9	20	6 AX295560	AX295560 Sequence
3	13.4	60.9	24	6 AX290927	AX290927 Sequence
4	13.4	60.9	24	6 AX290927	AX290927 Sequence
5	13	59.1	44	6 AR161400	AR161400 Sequence
6	13	59.1	44	6 AR161400	AR161400 Sequence
7	12.6	57.3	24	6 AX292255	AX292255 Sequence
8	12.6	57.3	24	6 AX292255	AX292255 Sequence
9	12.6	57.3	25	6 AX189358	AX189358 Sequence
10	12.6	57.3	25	6 AX189358	AX189358 Sequence
11	12.4	56.4	21	6 BD009441	BD009441 Probes, m
12	12.4	56.4	21	6 BD009441	BD009441 Probes, m
13	12.4	56.4	30	6 127040	127040 Sequence 61
14	12.4	56.4	30	6 127040	127040 Sequence 61
15	12.4	56.4	32	6 A41699	A41699 Sequence 26
16	12.4	56.4	32	6 A41699	A41699 Sequence 26
17	12.4	56.4	45	6 AX361282	AX361282 Sequence
18	12.4	56.4	45	6 AX361282	AX361282 Sequence
19	12.2	55.5	24	6 AX047302	AX047302 Sequence
20	12.2	55.5	24	6 AX047302	AX047302 Sequence
21	12.2	55.5	26	6 E06104	E06104 Oligonucleo
22	12.2	55.5	26	6 E06104	E06104 Oligonucleo
23	12.2	55.5	26	6 E10842	E10842 PCR primer
24	12.2	55.5	26	6 E10842	E10842 PCR primer
25	12.2	55.5	33	6 AR120578	AR120578 Sequence
26	12.2	55.5	33	6 AR120578	AR120578 Sequence
27	12.2	55.5	33	6 AR120579	AR120579 Sequence
28	12.2	55.5	33	6 AR120579	AR120579 Sequence
29	12.2	55.5	33	6 173498	173498 Sequence 1
30	12.2	55.5	33	6 173498	173498 Sequence 1
31	12.2	55.5	37	6 AX099887	AX099887 Sequence
32	12.2	55.5	37	6 AX099887	AX099887 Sequence
33	12.2	55.5	37	6 AX138008	AX138008 Sequence
34	12.2	55.5	37	6 AX138008	AX138008 Sequence
35	12.2	55.5	39	6 AR120598	AR120598 Sequence
36	12.2	55.5	39	6 AR120598	AR120598 Sequence
37	12.2	55.5	39	6 AR120599	AR120599 Sequence
38	12.2	55.5	39	6 AR120599	AR120599 Sequence
39	12.2	55.5	28	6 127047	127047 Sequence 68
40	12	54.5	28	6 127047	127047 Sequence 68
41	12	54.5	28	6 127048	127048 Sequence 69
42	12	54.5	28	6 127048	127048 Sequence 69
43	12	54.5	37	6 131695	131695 Sequence 3
44	12	54.5	37	6 131695	131695 Sequence 3
45	11.8	53.6	21	6 AX096000	AX096000 Sequence
46	11.8	53.6	21	6 AX096000	AX096000 Sequence
47	11.8	53.6	34	6 AR120591	AR120591 Sequence
48	11.8	53.6	34	6 AR120591	AR120591 Sequence
49	11.8	53.6	45	6 A13920	A13920 Nucleotide
50	11.8	53.6	45	6 A13920	A13920 Nucleotide
51	11.8	53.6	45	6 AR005067	AR005067 Sequence
52	11.8	53.6	45	6 AR005067	AR005067 Sequence
53	11.8	53.6	45	6 AR060883	AR060883 Sequence
54	11.8	53.6	45	6 AR060883	AR060883 Sequence
55	11.8	53.6	45	6 AR110817	AR110817 Sequence
56	11.8	53.6	45	6 AR110817	AR110817 Sequence
57	11.8	53.6	45	6 118296	118296 Sequence 43
58	11.8	53.6	45	6 118296	118296 Sequence 43
59	11.8	53.6	45	6 124509	124509 Sequence 41
60	11.8	53.6	45	6 124509	124509 Sequence 41
61	11.8	53.6	45	6 128903	128903 Sequence 41
62	11.8	53.6	45	6 128903	128903 Sequence 41
63	11.8	53.6	45	6 133041	133041 Sequence 41
64	11.8	53.6	45	6 133041	133041 Sequence 41
65	11.8	53.6	45	6 179637	179637 Sequence 41

C 66	11.8	53.6	45	6	179637	179637 Sequence 41	139	11.2	50.9	24	6	AR035478	AR035478 Sequence
C 67	11.6	52.7	21	6	BD009419	BD009419 Probes, m	C 140	11.2	50.9	24	6	AR035478	AR035478 Sequence
C 68	11.6	52.7	21	6	BD009419	BD009419 Probes, m	C 141	11.2	50.9	26	6	AX038074	AX038074 Sequence
C 69	11.6	52.7	38	6	AX218602	AX218602 Sequence	C 142	11.2	50.9	26	6	AX038074	AX038074 Sequence
C 70	11.6	52.7	38	6	AX218602	AX218602 Sequence	C 143	11.2	50.9	26	6	AX038075	AX038075 Sequence
C 71	11.6	52.7	48	6	117682	117682 Sequence 10	C 144	11.2	50.9	26	6	AX038075	AX038075 Sequence
C 72	11.6	52.7	48	6	117682	117682 Sequence 10	C 145	11.2	50.9	29	6	AR160337	AR160337 Sequence
C 73	11.4	51.8	18	6	AR058964	AR058964 Sequence	C 146	11.2	50.9	29	6	AR160337	AR160337 Sequence
C 74	11.4	51.8	18	6	AR058964	AR058964 Sequence	C 147	11.2	50.9	33	6	AX060822	AX060822 Sequence
C 75	11.4	51.8	18	6	AR058964	AR058964 Sequence	C 148	11.2	50.9	33	6	AX060822	AX060822 Sequence
C 76	11.4	51.8	18	6	AR105238	AR105238 Sequence	C 149	11.2	50.9	40	9	HS274607	HS274607 Sequence
C 77	11.4	51.8	18	6	AR119159	AR119159 Sequence	C 150	11.2	50.9	40	9	HS274607	HS274607 Sequence
C 78	11.4	51.8	18	6	AR119159	AR119159 Sequence	C 151	11.2	50.9	20	6	E06077	E06077 Sequence
C 79	11.4	51.8	18	6	AR123530	AR123530 Sequence	C 152	11.2	50.9	20	6	E06077	E06077 Sequence
C 80	11.4	51.8	18	6	AR123530	AR123530 Sequence	C 153	11.2	50.9	20	6	E08908	E08908 Sequence
C 81	11.4	51.8	18	6	AR123534	AR123534 Sequence	C 154	11.2	50.9	20	6	E08908	E08908 Sequence
C 82	11.4	51.8	18	6	AR123534	AR123534 Sequence	C 155	11.2	50.9	25	6	AX447652	AX447652 Sequence
C 83	11.4	51.8	18	6	AR138183	AR138183 Sequence	C 156	11.2	50.9	25	6	AX447652	AX447652 Sequence
C 84	11.4	51.8	18	6	AR138183	AR138183 Sequence	C 157	11.2	50.9	25	6	E41780	E41780 Sequence
C 85	11.4	51.8	18	6	AR176744	AR176744 Sequence	C 158	11.2	50.9	25	6	E41780	E41780 Sequence
C 86	11.4	51.8	18	6	AR176744	AR176744 Sequence	C 159	11.2	50.9	26	6	AX110707	AX110707 Sequence
C 87	11.4	51.8	18	6	AR198315	AR198315 Sequence	C 160	11.2	50.9	26	6	AX110707	AX110707 Sequence
C 88	11.4	51.8	18	6	AR198315	AR198315 Sequence	C 161	11.2	50.9	30	6	AX128544	AX128544 Sequence
C 89	11.4	51.8	18	6	AX470016	AX470016 Sequence	C 162	11.2	50.9	30	6	AX128544	AX128544 Sequence
C 90	11.4	51.8	18	6	AX470016	AX470016 Sequence	C 163	11.2	50.9	32	6	AR003442	AR003442 Sequence
C 91	11.4	51.8	27	6	BD012174	BD012174 Antineopl	C 164	11.2	50.9	32	6	AR003442	AR003442 Sequence
C 92	11.4	51.8	27	6	BD012174	BD012174 Antineopl	C 165	11.2	50.9	36	6	I31694	I31694 Sequence 2
C 93	11.4	51.8	27	23	BD004854	BD004854 Antineopl	C 166	11.2	50.9	36	6	I31694	I31694 Sequence 2
C 94	11.4	51.8	27	23	BD004854	BD004854 Antineopl	C 167	11.2	50.9	37	6	AR183323	AR183323 Sequence
C 95	11.4	51.8	29	6	AX192024	AX192024 Sequence	C 168	11.2	50.9	37	6	AR183323	AR183323 Sequence
C 96	11.4	51.8	29	6	AX192024	AX192024 Sequence	C 169	11.2	50.9	37	6	AX049947	AX049947 Sequence
C 97	11.4	51.8	38	6	BD011790	BD011790 RNP deriv	C 170	11.2	50.9	37	6	AX049947	AX049947 Sequence
C 98	11.4	51.8	38	6	BD011790	BD011790 RNP deriv	C 171	11.2	50.9	40	9	S80703	S80703 gamma delta
C 99	11.4	51.8	38	6	BD011791	BD011791 RNP deriv	C 172	11.2	50.9	40	9	S80703	S80703 gamma delta
C 100	11.4	51.8	38	6	BD011791	BD011791 RNP deriv	C 173	11.2	50.9	42	6	AI6704	AI6704 Oligonucleo
C 101	11.4	51.8	38	23	BD004187	BD004187 RNP deriv	C 174	11.2	50.9	43	6	AI6704	AI6704 Oligonucleo
C 102	11.4	51.8	38	23	BD004187	BD004187 RNP deriv	C 175	11.2	50.9	43	6	AX002956	AX002956 Sequence
C 103	11.4	51.8	38	23	BD004188	BD004188 RNP deriv	C 176	11.2	50.9	43	6	AX002956	AX002956 Sequence
C 104	11.4	51.8	38	23	BD004188	BD004188 RNP deriv	C 177	11.2	50.9	46	6	AR082253	AR082253 Sequence
C 105	11.4	51.8	39	6	AR148967	AR148967 Sequence	C 178	11.2	50.9	46	6	AR082253	AR082253 Sequence
C 106	11.4	51.8	39	6	AR148967	AR148967 Sequence	C 179	11.2	50.9	46	6	AR082276	AR082276 Sequence
C 107	11.4	51.8	39	6	AR196819	AR196819 Sequence	C 180	11.2	50.9	46	6	AR082276	AR082276 Sequence
C 108	11.4	51.8	39	6	AR196819	AR196819 Sequence	C 181	11.2	50.9	46	6	AR120795	AR120795 Sequence
C 109	11.4	51.8	40	6	E04063	E04063 PCR primer	C 182	11.2	50.9	46	6	AR120795	AR120795 Sequence
C 110	11.4	51.8	40	6	E04063	E04063 PCR primer	C 183	11.2	50.9	46	6	AR120818	AR120818 Sequence
C 111	11.4	51.8	40	6	E04071	E04071 Primer for	C 184	11.2	50.9	46	6	AR120818	AR120818 Sequence
C 112	11.4	51.8	40	6	E04071	E04071 Primer for	C 185	11.2	50.9	46	6	I78289	I78289 Sequence 97
C 113	11.4	51.8	41	6	AR096162	AR096162 Sequence	C 186	11.2	50.9	46	6	I78289	I78289 Sequence 97
C 114	11.4	51.8	41	6	AR096162	AR096162 Sequence	C 187	11.2	50.9	46	6	I78322	I78322 Sequence 12
C 115	11.4	51.8	41	6	AR096163	AR096163 Sequence	C 188	11.2	50.9	46	6	I78322	I78322 Sequence 12
C 116	11.4	51.8	41	6	AR096163	AR096163 Sequence	C 189	11.2	50.9	48	6	AX224371	AX224371 Sequence
C 117	11.4	51.8	41	6	AR210561	AR210561 Sequence	C 190	11.2	50.9	48	6	AX224371	AX224371 Sequence
C 118	11.4	51.8	41	6	AR210561	AR210561 Sequence	C 191	11.2	50.9	48	6	I40773	I40773 Sequence 10
C 119	11.4	51.8	41	6	AR210562	AR210562 Sequence	C 192	11.2	50.9	48	6	I40773	I40773 Sequence 10
C 120	11.4	51.8	41	6	AR210562	AR210562 Sequence	C 193	10.8	49.1	20	6	AR067377	AR067377 Sequence
C 121	11.4	51.8	45	6	AX361281	AX361281 Sequence	C 194	10.8	49.1	20	6	AR067377	AR067377 Sequence
C 122	11.4	51.8	45	6	AX361281	AX361281 Sequence	C 195	10.8	49.1	22	6	A38334	A38334 Sequence 7
C 123	11.4	51.8	47	6	AR170381	AR170381 Sequence	C 196	10.8	49.1	22	6	A38334	A38334 Sequence 7
C 124	11.4	51.8	47	6	AR170381	AR170381 Sequence	C 197	10.8	49.1	26	6	AX481669	AX481669 Sequence
C 125	11.4	51.8	48	6	AR021432	AR021432 Sequence	C 198	10.8	49.1	26	6	AX481669	AX481669 Sequence
C 126	11.4	51.8	48	6	AR021432	AR021432 Sequence	C 199	10.8	49.1	28	6	AX57117	AX57117 Sequence 13
C 127	11.4	51.8	48	6	AR042994	AR042994 Sequence	C 200	10.8	49.1	28	6	AX57117	AX57117 Sequence 13
C 128	11.4	51.8	48	6	AR042994	AR042994 Sequence	C 201	10.8	49.1	28	6	A57118	A57118 Sequence 14
C 129	11.4	51.8	48	6	AR161328	AR161328 Sequence	C 202	10.8	49.1	28	6	A57118	A57118 Sequence 14
C 130	11.4	51.8	48	6	AR161328	AR161328 Sequence	C 203	10.8	49.1	28	6	AX153831	AX153831 Sequence
C 131	11.4	51.8	48	6	I43973	I43973 Sequence, 64	C 204	10.8	49.1	28	6	AX153831	AX153831 Sequence
C 132	11.4	51.8	48	6	I43973	I43973 Sequence, 64	C 205	10.8	49.1	29	6	A31175	A31175 DNA fragmen
C 133	11.4	51.8	48	6	I62985	I62985 Sequence 11	C 206	10.8	49.1	29	6	A31175	A31175 DNA fragmen
C 134	11.4	51.8	48	6	I62985	I62985 Sequence 11	C 207	10.8	49.1	34	6	AR091730	AR091730 Sequence
C 135	11.4	51.8	48	6	I62985	I62985 Sequence 11	C 208	10.8	49.1	34	6	AR091730	AR091730 Sequence
C 136	11.4	51.8	48	6	I88738	I88738 Sequence 11	C 209	10.8	49.1	40	6	AR069956	AR069956 Sequence
C 137	11.2	50.9	20	6	AX298397	AX298397 Sequence	C 210	10.8	49.1	40	6	AR069956	AR069956 Sequence
C 138	11.2	50.9	20	6	AX298397	AX298397 Sequence	C 211	10.8	49.1	40	6	AR076090	AR076090 Sequence

C 212	10.8	49.1	40	6	AR076090	AR076090 Sequence	285	10.6	48.2	25	6	E44264	E44264 Oligo-DNA s
C 213	10.8	49.1	40	6	BD007642	BD007642 Process f	286	10.6	48.2	25	6	E44264	E44264 Oligo-DNA s
C 214	10.8	49.1	40	6	BD007642	BD007642 Process f	287	10.6	48.2	26	6	BD000266	BD000266 Oligonuc1
C 215	10.8	49.1	41	6	AX113779	AX113779 Sequence	288	10.6	48.2	26	6	BD000266	BD000266 Oligonuc1
C 216	10.8	49.1	41	6	AX113779	AX113779 Sequence	289	10.6	48.2	27	6	AX036874	AX036874 Sequence
C 217	10.8	49.1	45	6	AJ3049	AJ3049 Id-phoA1a16	290	10.6	48.2	27	6	AX036874	AX036874 Sequence
C 218	10.8	49.1	45	6	AJ3049	AJ3049 Id-phoA1a16	291	10.6	48.2	27	6	AX083709	AX083709 Sequence
C 219	10.8	49.1	48	6	AR069955	AR069955 Sequence	292	10.6	48.2	27	6	AX083709	AX083709 Sequence
C 220	10.8	49.1	48	6	AR069955	AR069955 Sequence	293	10.6	48.2	29	6	AX253007	AX253007 Sequence
C 221	10.8	49.1	48	6	AR076089	AR076089 Sequence	294	10.6	48.2	29	6	AX253007	AX253007 Sequence
C 222	10.8	49.1	48	6	AR076089	AR076089 Sequence	295	10.6	48.2	30	6	A58136	A58136 Sequence 28
C 223	10.8	49.1	48	6	BD007641	BD007641 Process f	296	10.6	48.2	30	6	A58136	A58136 Sequence 28
C 224	10.8	49.1	48	6	BD007641	BD007641 Process f	297	10.6	48.2	30	6	BD012180	BD012180 Antineopl
C 225	10.8	49.1	50	6	AX093086	AX093086 Sequence	298	10.6	48.2	30	6	BD012180	BD012180 Antineopl
C 226	10.8	49.1	50	6	AX093086	AX093086 Sequence	299	10.6	48.2	30	6	E04686	E04686 Synthetic n
C 227	10.8	49.1	50	6	AX093090	AX093090 Sequence	300	10.6	48.2	30	6	E04686	E04686 Synthetic n
C 228	10.8	49.1	50	6	AX093090	AX093090 Sequence	301	10.6	48.2	30	23	BD004860	BD004860 Antineopl
C 229	10.6	48.2	18	6	A70959	A70959 Sequence 13	302	10.6	48.2	30	23	BD004860	BD004860 Antineopl
C 230	10.6	48.2	18	6	A70959	A70959 Sequence 13	303	10.6	48.2	31	6	AX480656	AX480656 Sequence
C 231	10.6	48.2	20	6	AR031036	AR031036 Sequence	304	10.6	48.2	31	6	AX480656	AX480656 Sequence
C 232	10.6	48.2	20	6	AR031036	AR031036 Sequence	305	10.6	48.2	31	6	AX480657	AX480657 Sequence
C 233	10.6	48.2	20	6	AR139569	AR139569 Sequence	306	10.6	48.2	31	6	AX480657	AX480657 Sequence
C 234	10.6	48.2	20	6	AR139569	AR139569 Sequence	307	10.6	48.2	31	6	E50123	E50123 Porous ho11
C 235	10.6	48.2	20	6	AR167032	AR167032 Sequence	308	10.6	48.2	31	6	E50123	E50123 Porous ho11
C 236	10.6	48.2	20	6	AR167032	AR167032 Sequence	309	10.6	48.2	32	6	AR212127	AR212127 Sequence
C 237	10.6	48.2	20	6	AR210687	AR210687 Sequence	310	10.6	48.2	32	6	AR212127	AR212127 Sequence
C 238	10.6	48.2	20	6	AR210687	AR210687 Sequence	311	10.6	48.2	34	6	AX282130	AX282130 Sequence
C 239	10.6	48.2	20	11	DOGC00607A	L77547 Canis fam11	312	10.6	48.2	34	6	AX282130	AX282130 Sequence
C 240	10.6	48.2	20	11	DOGC00607A	L77547 Canis fam11	313	10.6	48.2	34	6	AX282239	AX282239 Sequence
C 241	10.6	48.2	20	12	AB068715	AB068715 Synthetic	314	10.6	48.2	34	6	AX282239	AX282239 Sequence
C 242	10.6	48.2	20	12	AB068715	AB068715 Synthetic	315	10.6	48.2	34	6	AX322890	AX322890 Sequence
C 243	10.6	48.2	21	6	A68285	A68285 Sequence 6	316	10.6	48.2	34	6	AX322890	AX322890 Sequence
C 244	10.6	48.2	21	6	A68285	A68285 Sequence 6	317	10.6	48.2	36	6	A70977	A70977 Sequence 31
C 245	10.6	48.2	21	6	A68350	A68350 Sequence 9	318	10.6	48.2	36	6	A70977	A70977 Sequence 31
C 246	10.6	48.2	21	6	A68350	A68350 Sequence 9	319	10.6	48.2	37	6	AX002959	AX002959 Sequence
C 247	10.6	48.2	21	6	AR007281	AR007281 Sequence	320	10.6	48.2	37	6	AX002959	AX002959 Sequence
C 248	10.6	48.2	21	6	AR007281	AR007281 Sequence	321	10.6	48.2	37	6	AX135989	AX135989 Sequence
C 249	10.6	48.2	21	6	AR062700	AR062700 Sequence	322	10.6	48.2	37	6	AX135989	AX135989 Sequence
C 250	10.6	48.2	21	6	AR062700	AR062700 Sequence	323	10.6	48.2	37	6	AX136046	AX136046 Sequence
C 251	10.6	48.2	21	6	AR154843	AR154843 Sequence	324	10.6	48.2	37	6	AX136046	AX136046 Sequence
C 252	10.6	48.2	21	6	AR154843	AR154843 Sequence	325	10.6	48.2	37	6	BD006881	BD006881 Oligonuc1
C 253	10.6	48.2	21	6	AR170540	AR170540 Sequence	326	10.6	48.2	37	6	BD006881	BD006881 Oligonuc1
C 254	10.6	48.2	21	6	AR170540	AR170540 Sequence	327	10.6	48.2	37	6	E25770	E25770 Method for
C 255	10.6	48.2	21	6	AR170704	AR170704 Sequence	328	10.6	48.2	37	6	E25770	E25770 Method for
C 256	10.6	48.2	21	6	AR170704	AR170704 Sequence	329	10.6	48.2	37	9	AB055780	AB055780 Homo sapi
C 257	10.6	48.2	21	6	AR174772	AR174772 Sequence	330	10.6	48.2	37	9	AB055780	AB055780 Homo sapi
C 258	10.6	48.2	21	6	AR174772	AR174772 Sequence	331	10.6	48.2	38	6	AX218870	AX218870 Sequence
C 259	10.6	48.2	21	6	E65368	E65368 Genome DNA	332	10.6	48.2	38	6	AX218870	AX218870 Sequence
C 260	10.6	48.2	21	6	E65368	E65368 Genome DNA	333	10.6	48.2	38	6	AX423905	AX423905 Sequence
C 261	10.6	48.2	22	6	105640	105640 Sequence 13	334	10.6	48.2	38	6	AX423905	AX423905 Sequence
C 262	10.6	48.2	22	6	105640	105640 Sequence 13	335	10.6	48.2	38	6	AX423939	AX423939 Sequence
C 263	10.6	48.2	23	6	AX057257	AX057257 Sequence	336	10.6	48.2	38	6	AX423939	AX423939 Sequence
C 264	10.6	48.2	23	6	AX057257	AX057257 Sequence	337	10.6	48.2	38	6	114878	114878 Sequence 5
C 265	10.6	48.2	24	6	AR103724	AR103724 Sequence	338	10.6	48.2	38	6	114878	114878 Sequence 5
C 266	10.6	48.2	24	6	AR103724	AR103724 Sequence	339	10.6	48.2	38	6	192688	192688 Sequence 5
C 267	10.6	48.2	24	6	AR175413	AR175413 Sequence	340	10.6	48.2	38	6	192688	192688 Sequence 5
C 268	10.6	48.2	24	6	AR175413	AR175413 Sequence	341	10.6	48.2	39	6	A38384	A38384 Sequence 19
C 269	10.6	48.2	24	6	AX110657	AX110657 Sequence	342	10.6	48.2	39	6	A38384	A38384 Sequence 19
C 270	10.6	48.2	24	6	AX110657	AX110657 Sequence	343	10.6	48.2	39	6	AR117907	AR117907 Sequence
C 271	10.6	48.2	24	6	AX250662	AX250662 Sequence	344	10.6	48.2	39	6	AR117907	AR117907 Sequence
C 272	10.6	48.2	24	6	AX250662	AX250662 Sequence	345	10.6	48.2	39	6	174385	174385 Sequence 19
C 273	10.6	48.2	24	6	AX419900	AX419900 Sequence	346	10.6	48.2	39	6	174385	174385 Sequence 19
C 274	10.6	48.2	24	6	AX419900	AX419900 Sequence	347	10.6	48.2	40	9	S80741	S80741 gamma delta
C 275	10.6	48.2	24	6	AX444788	AX444788 Sequence	348	10.6	48.2	40	9	S80741	S80741 gamma delta
C 276	10.6	48.2	24	6	AX444788	AX444788 Sequence	349	10.6	48.2	42	6	AX033806	AX033806 Sequence
C 277	10.6	48.2	25	6	BD000246	BD000246 Oligonuc1	350	10.6	48.2	42	6	AX033806	AX033806 Sequence
C 278	10.6	48.2	25	6	BD000246	BD000246 Oligonuc1	351	10.6	48.2	45	6	AR168037	AR168037 Sequence
C 279	10.6	48.2	25	6	BD000255	BD000255 Oligonuc1	352	10.6	48.2	45	6	AR168037	AR168037 Sequence
C 280	10.6	48.2	25	6	BD000255	BD000255 Oligonuc1	353	10.6	48.2	45	6	AR204808	AR204808 Sequence
C 281	10.6	48.2	25	6	BD000264	BD000264 Oligonuc1	354	10.6	48.2	45	6	AR204808	AR204808 Sequence
C 282	10.6	48.2	25	6	BD000264	BD000264 Oligonuc1	355	10.6	48.2	47	6	AR179591	AR179591 Sequence
C 283	10.6	48.2	25	6	E44263	E44263 Oligo-DNA s	356	10.6	48.2	47	6	AR179591	AR179591 Sequence
C 284	10.6	48.2	25	6	E44263	E44263 Oligo-DNA s	357	10.6	48.2	48	6	AR076907	AR076907 Sequence

C 358	10.6	48.2	48	6	AR076907	AR076907 Sequence	C 431	10.4	47.3	24	6	AX355778	AX355778 Sequence
C 359	10.6	48.2	48	6	AR076912	AR076912 Sequence	C 432	10.4	47.3	24	6	AX355778	AX355778 Sequence
C 360	10.6	48.2	48	6	AR076912	AR076912 Sequence	C 433	10.4	47.3	24	6	AX447335	AX447335 Sequence
C 361	10.6	48.2	48	6	AR167298	AR167298 Sequence	C 434	10.4	47.3	24	6	AX447335	AX447335 Sequence
C 362	10.6	48.2	48	6	AR167298	AR167298 Sequence	C 435	10.4	47.3	26	6	AR090772	AR090772 Sequence
C 363	10.6	48.2	48	6	AR167303	AR167303 Sequence	C 436	10.4	47.3	26	6	AR090772	AR090772 Sequence
C 364	10.6	48.2	48	6	AR167303	AR167303 Sequence	C 437	10.4	47.3	26	6	AR197807	AR197807 Sequence
C 365	10.6	48.2	50	1	FVBFOKIF	M18010 Flavobacter	C 438	10.4	47.3	26	6	AR197807	AR197807 Sequence
C 366	10.6	48.2	50	1	FVBFOKIF	M18010 Flavobacter	C 439	10.4	47.3	26	6	AX463156	AX463156 Sequence
C 367	10.6	48.2	50	6	AR028065	AR028065 Sequence	C 440	10.4	47.3	26	6	AX463156	AX463156 Sequence
C 368	10.6	48.2	50	6	AR028065	AR028065 Sequence	C 441	10.4	47.3	27	6	AX115612	AX115612 Sequence
C 369	10.6	48.2	50	6	BD000119	BD000119 Nucleic a	C 442	10.4	47.3	27	6	AX115612	AX115612 Sequence
C 370	10.6	48.2	50	6	BD000119	BD000119 Nucleic a	C 443	10.4	47.3	28	6	AX115390	AX115390 Sequence
C 371	10.6	48.2	50	6	BD004784	BD004784 Method of	C 444	10.4	47.3	28	6	AX115390	AX115390 Sequence
C 372	10.6	48.2	50	6	BD004784	BD004784 Method of	C 445	10.4	47.3	28	6	AR006745	AR006745 Sequence
C 373	10.6	48.2	50	6	BD006778	BD006778 Method fo	C 446	10.4	47.3	29	6	AR006745	AR006745 Sequence
C 374	10.6	48.2	50	6	BD006778	BD006778 Method fo	C 447	10.4	47.3	29	6	AR032021	AR032021 Sequence
C 375	10.6	48.2	50	6	E44267	E44267 Oligo-DNA s	C 448	10.4	47.3	29	6	AR032021	AR032021 Sequence
C 376	10.6	48.2	50	6	E44267	E44267 Oligo-DNA s	C 449	10.4	47.3	29	6	AR038517	AR038517 Sequence
C 377	10.6	48.2	50	6	E44268	E44268 Oligo-DNA s	C 450	10.4	47.3	29	6	AR038517	AR038517 Sequence
C 378	10.6	48.2	50	6	E44268	E44268 Oligo-DNA s	C 451	10.4	47.3	29	6	AR050864	AR050864 Sequence
C 379	10.6	48.2	50	6	E44269	E44269 Oligo-DNA s	C 452	10.4	47.3	29	6	AR050864	AR050864 Sequence
C 380	10.6	48.2	50	6	E44269	E44269 Oligo-DNA s	C 453	10.4	47.3	29	6	AX319796	AX319796 Sequence
C 381	10.6	48.2	50	6	E50439	E50439 Method for	C 454	10.4	47.3	29	6	AX319796	AX319796 Sequence
C 382	10.6	48.2	50	6	E50439	E50439 Method for	C 455	10.4	47.3	29	6	E05890	E05890 Primer. 9/1
C 383	10.4	47.3	14	6	I06036	I06036 Sequence 5	C 456	10.4	47.3	29	6	E05890	E05890 Primer. 9/1
C 384	10.4	47.3	14	6	I06036	I06036 Sequence 5	C 457	10.4	47.3	29	6	E07921	E07921 Primer. 9/1
C 385	10.4	47.3	14	6	I06041	I06041 Sequence 10	C 458	10.4	47.3	29	6	E07921	E07921 Primer. 9/1
C 386	10.4	47.3	14	6	I06041	I06041 Sequence 10	C 459	10.4	47.3	30	6	AX007150	AX007150 Sequence
C 387	10.4	47.3	14	6	I06042	I06042 Sequence 11	C 460	10.4	47.3	30	6	AX007150	AX007150 Sequence
C 388	10.4	47.3	14	6	I06042	I06042 Sequence 11	C 461	10.4	47.3	30	6	AX008215	AX008215 Sequence
C 389	10.4	47.3	18	6	AR130097	AR130097 Sequence	C 462	10.4	47.3	30	6	AX008215	AX008215 Sequence
C 390	10.4	47.3	18	6	AR130097	AR130097 Sequence	C 463	10.4	47.3	31	6	A38545	A38545 Sequence 5
C 391	10.4	47.3	20	6	AR029388	AR029388 Sequence	C 464	10.4	47.3	31	6	A38545	A38545 Sequence 5
C 392	10.4	47.3	20	6	AR029388	AR029388 Sequence	C 465	10.4	47.3	31	6	A67246	A67246 Sequence 2
C 393	10.4	47.3	20	6	AX293756	AX293756 Sequence	C 466	10.4	47.3	31	6	A67246	A67246 Sequence 2
C 394	10.4	47.3	20	6	AX293756	AX293756 Sequence	C 467	10.4	47.3	31	6	A94762	A94762 Sequence 6
C 395	10.4	47.3	20	6	AX293909	AX293909 Sequence	C 468	10.4	47.3	31	6	A94762	A94762 Sequence 6
C 396	10.4	47.3	20	6	AX293909	AX293909 Sequence	C 469	10.4	47.3	31	6	AR013839	AR013839 Sequence
C 397	10.4	47.3	20	6	AX402157	AX402157 Sequence	C 470	10.4	47.3	31	6	AR013839	AR013839 Sequence
C 398	10.4	47.3	20	6	AX402157	AX402157 Sequence	C 471	10.4	47.3	31	6	AR033793	AR033793 Sequence
C 399	10.4	47.3	20	6	AX402158	AX402158 Sequence	C 472	10.4	47.3	31	6	AR033793	AR033793 Sequence
C 400	10.4	47.3	20	6	AX402158	AX402158 Sequence	C 473	10.4	47.3	31	6	AR042453	AR042453 Sequence
C 401	10.4	47.3	20	6	BD004094	BD004094 Apoptosis	C 474	10.4	47.3	31	6	AR042453	AR042453 Sequence
C 402	10.4	47.3	20	6	BD004094	BD004094 Apoptosis	C 475	10.4	47.3	31	6	AR058333	AR058333 Sequence
C 403	10.4	47.3	20	6	I17925	I17925 Sequence 5	C 476	10.4	47.3	31	6	AR058333	AR058333 Sequence
C 404	10.4	47.3	20	6	I17925	I17925 Sequence 5	C 477	10.4	47.3	31	6	AR088159	AR088159 Sequence
C 405	10.4	47.3	21	6	A22397	A22397 Oligonucleo	C 478	10.4	47.3	31	6	AR088159	AR088159 Sequence
C 406	10.4	47.3	21	6	A22397	A22397 Oligonucleo	C 479	10.4	47.3	31	6	AR131296	AR131296 Sequence
C 407	10.4	47.3	21	6	AX369420	AX369420 Sequence	C 480	10.4	47.3	31	6	AR131296	AR131296 Sequence
C 408	10.4	47.3	21	6	AX369420	AX369420 Sequence	C 481	10.4	47.3	31	6	AR173194	AR173194 Sequence
C 409	10.4	47.3	21	6	E04564	E04564 PCR primer	C 482	10.4	47.3	31	6	AR173194	AR173194 Sequence
C 410	10.4	47.3	21	6	E04564	E04564 PCR primer	C 483	10.4	47.3	31	6	BD002474	BD002474 Gene comp
C 411	10.4	47.3	21	6	E05239	E05239 Part of DNA	C 484	10.4	47.3	31	6	BD002474	BD002474 Gene comp
C 412	10.4	47.3	21	6	E05239	E05239 Part of DNA	C 485	10.4	47.3	33	6	AR171835	AR171835 Sequence
C 413	10.4	47.3	21	6	E05255	E05255 Primer for	C 486	10.4	47.3	33	6	AR171835	AR171835 Sequence
C 414	10.4	47.3	21	6	E05255	E05255 Primer for	C 487	10.4	47.3	33	6	AX148590	AX148590 Sequence
C 415	10.4	47.3	21	6	I22223	I22223 Sequence 4	C 488	10.4	47.3	33	6	AX148590	AX148590 Sequence
C 416	10.4	47.3	21	6	I22223	I22223 Sequence 4	C 489	10.4	47.3	33	6	I86950	I86950 Sequence 39
C 417	10.4	47.3	21	6	I22226	I22226 Sequence 7	C 490	10.4	47.3	33	6	I86950	I86950 Sequence 39
C 418	10.4	47.3	21	6	I22226	I22226 Sequence 7	C 491	10.4	47.3	33	6	I95606	I95606 Sequence 21
C 419	10.4	47.3	21	14	PPHSRPHRA	M64810 Human papil	C 492	10.4	47.3	33	6	I95606	I95606 Sequence 21
C 420	10.4	47.3	21	14	PPHSRPHRA	M64810 Human papil	C 493	10.4	47.3	35	6	A31401	A31401 Salt-HindII
C 421	10.4	47.3	22	6	AR127459	AR127459 Sequence	C 494	10.4	47.3	35	6	A31401	A31401 Salt-HindII
C 422	10.4	47.3	22	6	AR127459	AR127459 Sequence	C 495	10.4	47.3	36	6	A08036	A08036 Oligonucleo
C 423	10.4	47.3	23	6	AX082405	AX082405 Sequence	C 496	10.4	47.3	36	6	A08036	A08036 Oligonucleo
C 424	10.4	47.3	23	6	AX082405	AX082405 Sequence	C 497	10.4	47.3	36	6	A31402	A31402 Salt-HindII
C 425	10.4	47.3	24	6	AX104645	AX104645 Sequence	C 498	10.4	47.3	36	6	A31402	A31402 Salt-HindII
C 426	10.4	47.3	24	6	AX104645	AX104645 Sequence	C 499	10.4	47.3	36	6	AR034005	AR034005 Sequence
C 427	10.4	47.3	24	6	AX289123	AX289123 Sequence	C 500	10.4	47.3	36	6	AR034005	AR034005 Sequence
C 428	10.4	47.3	24	6	AX289123	AX289123 Sequence	C 501	10.4	47.3	36	6	AR124014	AR124014 Sequence
C 429	10.4	47.3	24	6	AX289276	AX289276 Sequence	C 502	10.4	47.3	36	6	AR124014	AR124014 Sequence
C 430	10.4	47.3	24	6	AX289276	AX289276 Sequence	C 503	10.4	47.3	37	6	I31696	I31696 Sequence 4

C 504	10.4	47.3	37	6	I31696	I31696 Sequence 4	577	10.2	46.4	24	6	AR162030	AR162030 Sequence
C 505	10.4	47.3	38	6	AX319802	AX319802 Sequence	C 578	10.2	46.4	24	6	AR162030	AR162030 Sequence
C 506	10.4	47.3	38	6	AX319802	AX319802 Sequence	C 579	10.2	46.4	24	6	AR162030	AR162030 Sequence
C 507	10.4	47.3	39	6	AR118505	AR118505 Sequence	C 580	10.2	46.4	24	6	AX289037	AX289037 Sequence
C 508	10.4	47.3	39	6	AR118505	AR118505 Sequence	C 581	10.2	46.4	24	6	AX289291	AX289291 Sequence
C 509	10.4	47.3	40	6	A75559	A75559 Sequence 1	C 582	10.2	46.4	24	6	AX289291	AX289291 Sequence
C 510	10.4	47.3	40	6	A75559	A75559 Sequence 1	C 583	10.2	46.4	24	6	AX289361	AX289361 Sequence
C 511	10.4	47.3	40	6	A75560	A75560 Sequence 1	C 584	10.2	46.4	24	6	AX289361	AX289361 Sequence
C 512	10.4	47.3	40	6	A75560	A75560 Sequence 1	C 585	10.2	46.4	24	6	AX290805	AX290805 Sequence
C 513	10.4	47.3	40	6	AR044603	AR044603 Sequence	C 586	10.2	46.4	24	6	AX290805	AX290805 Sequence
C 514	10.4	47.3	40	6	AR044603	AR044603 Sequence	C 587	10.2	46.4	24	6	AX292518	AX292518 Sequence
C 515	10.4	47.3	40	6	AX456282	AX456282 Sequence	C 588	10.2	46.4	24	6	AX292518	AX292518 Sequence
C 516	10.4	47.3	40	6	AX456282	AX456282 Sequence	C 589	10.2	46.4	24	6	AX292518	AX292518 Sequence
C 517	10.4	47.3	40	6	E05433	E05433 Oligonucleo	C 590	10.2	46.4	24	6	AX292871	AX292871 Sequence
C 518	10.4	47.3	40	6	E05433	E05433 Oligonucleo	C 591	10.2	46.4	24	6	AX292871	AX292871 Sequence
C 519	10.4	47.3	40	6	I13133	I13133 Sequence 12	C 592	10.2	46.4	24	6	I03297	I03297 Sequence 1
C 520	10.4	47.3	40	6	I13133	I13133 Sequence 12	C 593	10.2	46.4	24	6	AX477105	AX477105 Sequence
C 521	10.4	47.3	40	6	I36492	I36492 Sequence 12	C 594	10.2	46.4	26	6	AX477105	AX477105 Sequence
C 522	10.4	47.3	43	6	I36492	I36492 Sequence 12	C 595	10.2	46.4	27	6	I73504	I73504 Sequence 7
C 523	10.4	47.3	43	6	I78653	I78653 Sequence 8	C 596	10.2	46.4	27	6	I73504	I73504 Sequence 7
C 524	10.4	47.3	43	6	I78653	I78653 Sequence 8	C 597	10.2	46.4	28	6	AX060371	AX060371 Sequence
C 525	10.4	47.3	43	6	I78654	I78654 Sequence 9	C 598	10.2	46.4	28	6	AX060371	AX060371 Sequence
C 526	10.4	47.3	43	6	I78654	I78654 Sequence 9	C 599	10.2	46.4	28	6	AX085435	AX085435 Sequence
C 527	10.4	47.3	46	12	SYNBRWF	M94408 Artificial	C 600	10.2	46.4	28	6	AX085435	AX085435 Sequence
C 528	10.4	47.3	46	12	SYNBRWF	M94408 Artificial	C 601	10.2	46.4	28	6	AX085435	AX085435 Sequence
C 529	10.4	47.3	48	6	AR020972	AR020972 Sequence	C 602	10.2	46.4	28	6	AX202163	AX202163 Sequence
C 530	10.4	47.3	48	6	AR020972	AR020972 Sequence	C 603	10.2	46.4	29	6	AX202163	AX202163 Sequence
C 531	10.4	47.3	48	6	AR043387	AR043387 Sequence	C 604	10.2	46.4	29	6	AR151653	AR151653 Sequence
C 532	10.4	47.3	48	6	AR043387	AR043387 Sequence	C 605	10.2	46.4	29	6	AR151653	AR151653 Sequence
C 533	10.4	47.3	48	6	AR062302	AR062302 Sequence	C 606	10.2	46.4	30	6	A39579	A39579 Sequence 18
C 534	10.4	47.3	48	6	AR062302	AR062302 Sequence	C 607	10.2	46.4	30	6	A39579	A39579 Sequence 18
C 535	10.4	47.3	48	6	AR183761	AR183761 Sequence	C 608	10.2	46.4	30	6	A58134	A58134 Sequence 26
C 536	10.4	47.3	48	6	AR183761	AR183761 Sequence	C 609	10.2	46.4	30	6	A58134	A58134 Sequence 26
C 537	10.4	47.3	48	6	AX076971	AX076971 Sequence	C 610	10.2	46.4	30	6	A93166	A93166 Sequence 18
C 538	10.4	47.3	48	6	AX076971	AX076971 Sequence	C 611	10.2	46.4	30	6	A93166	A93166 Sequence 18
C 539	10.4	47.3	48	6	AX299782	AX299782 Sequence	C 612	10.2	46.4	30	6	AR082500	AR082500 Sequence
C 540	10.4	47.3	48	6	AX299782	AX299782 Sequence	C 613	10.2	46.4	30	6	AR082500	AR082500 Sequence
C 541	10.2	46.4	18	6	AX352188	AX352188 Sequence	C 614	10.2	46.4	30	6	AR159658	AR159658 Sequence
C 542	10.2	46.4	18	6	AX352188	AX352188 Sequence	C 615	10.2	46.4	30	6	AR159658	AR159658 Sequence
C 543	10.2	46.4	20	6	AR074417	AR074417 Sequence	C 616	10.2	46.4	30	6	AX036915	AX036915 Sequence
C 544	10.2	46.4	20	6	AR074417	AR074417 Sequence	C 617	10.2	46.4	30	6	AX036915	AX036915 Sequence
C 545	10.2	46.4	20	6	AR173216	AR173216 Sequence	C 618	10.2	46.4	30	6	AX306644	AX306644 Sequence
C 546	10.2	46.4	20	6	AR173216	AR173216 Sequence	C 619	10.2	46.4	33	6	AR004392	AR004392 Sequence
C 547	10.2	46.4	20	6	AR174795	AR174795 Sequence	C 620	10.2	46.4	33	6	AR004392	AR004392 Sequence
C 548	10.2	46.4	20	6	AR174795	AR174795 Sequence	C 621	10.2	46.4	33	6	AR064954	AR064954 Sequence
C 549	10.2	46.4	20	6	AX293994	AX293994 Sequence	C 622	10.2	46.4	33	6	AR064954	AR064954 Sequence
C 550	10.2	46.4	20	6	AX293994	AX293994 Sequence	C 623	10.2	46.4	33	6	AR097184	AR097184 Sequence
C 551	10.2	46.4	20	6	AX297151	AX297151 Sequence	C 624	10.2	46.4	33	6	AR097184	AR097184 Sequence
C 552	10.2	46.4	20	6	AX297151	AX297151 Sequence	C 625	10.2	46.4	33	6	AR130682	AR130682 Sequence
C 553	10.2	46.4	20	6	E05254	E05254 Primer for	C 626	10.2	46.4	33	6	AR130682	AR130682 Sequence
C 554	10.2	46.4	20	6	E05254	E05254 Primer for	C 627	10.2	46.4	33	6	AR172031	AR172031 Sequence
C 555	10.2	46.4	20	6	E11071	E11071 Primer. 9/1	C 628	10.2	46.4	33	6	AR172031	AR172031 Sequence
C 556	10.2	46.4	20	6	E11071	E11071 Primer. 9/1	C 629	10.2	46.4	33	6	I82867	I82867 Sequence 46
C 557	10.2	46.4	21	6	E05231	E05231 Part of DNA	C 630	10.2	46.4	33	6	I82867	I82867 Sequence 46
C 558	10.2	46.4	21	6	E05231	E05231 Part of DNA	C 631	10.2	46.4	36	6	I31693	I31693 Sequence 1
C 559	10.2	46.4	21	6	E05235	E05235 Part of DNA	C 632	10.2	46.4	36	6	I31693	I31693 Sequence 1
C 560	10.2	46.4	21	6	E05235	E05235 Part of DNA	C 633	10.2	46.4	36	6	I62073	I62073 Sequence 62
C 561	10.2	46.4	21	6	E06293	E06293 Primer. 9/1	C 634	10.2	46.4	36	6	I62073	I62073 Sequence 62
C 562	10.2	46.4	21	6	E06293	E06293 Primer. 9/1	C 635	10.2	46.4	36	6	I77522	I77522 Sequence 22
C 563	10.2	46.4	21	6	E06489	E06489 Primer. 9/1	C 636	10.2	46.4	36	6	I77522	I77522 Sequence 22
C 564	10.2	46.4	21	6	E06489	E06489 Primer. 9/1	C 637	10.2	46.4	36	6	I78056	I78056 Sequence 76
C 565	10.2	46.4	22	6	AX104783	AX104783 Sequence	C 638	10.2	46.4	37	6	I78056	I78056 Sequence 76
C 566	10.2	46.4	22	6	AX104783	AX104783 Sequence	C 639	10.2	46.4	37	6	AX107345	AX107345 Sequence
C 567	10.2	46.4	22	6	AX104853	AX104853 Sequence	C 640	10.2	46.4	37	6	AX107345	AX107345 Sequence
C 568	10.2	46.4	22	6	AX104853	AX104853 Sequence	C 641	10.2	46.4	38	6	AR046531	AR046531 Sequence
C 569	10.2	46.4	22	6	AX105128	AX105128 Sequence	C 642	10.2	46.4	38	6	AR046531	AR046531 Sequence
C 570	10.2	46.4	22	6	AX105128	AX105128 Sequence	C 643	10.2	46.4	38	6	AX036914	AX036914 Sequence
C 571	10.2	46.4	23	6	AR153842	AR153842 Sequence	C 644	10.2	46.4	38	6	AX036914	AX036914 Sequence
C 572	10.2	46.4	23	6	AR153842	AR153842 Sequence	C 645	10.2	46.4	38	6	AX201776	AX201776 Sequence
C 573	10.2	46.4	23	6	AX020841	AX020841 Sequence	C 646	10.2	46.4	38	6	AX201776	AX201776 Sequence
C 574	10.2	46.4	23	6	AX020841	AX020841 Sequence	C 647	10.2	46.4	38	6	AX218869	AX218869 Sequence
C 575	10.2	46.4	24	6	A41226	A41226 Sequence 10	C 648	10.2	46.4	38	6	AX218869	AX218869 Sequence
C 576	10.2	46.4	24	6	A41226	A41226 Sequence 10	C 649	10.2	46.4	38	6	AX273501	AX273501 Sequence

C 650	10.2	46.4	38	6	AX273501	AX273501 Sequence	723	10	45.5	24	6	AX444718	AX444718 Sequence
C 651	10.2	46.4	38	6	I53583	I53583 Sequence 13	C 724	10	45.5	24	6	AX444718	AX444718 Sequence
C 652	10.2	46.4	38	6	I53583	I53583 Sequence 13	C 725	10	45.5	24	6	I24200	I24200 Sequence 22
C 653	10.2	46.4	39	6	A11980	A11980 Sequence 21	C 726	10	45.5	24	6	I24200	I24200 Sequence 22
C 654	10.2	46.4	39	6	A11980	A11980 Sequence 21	C 727	10	45.5	25	6	AR034944	AR034944 Sequence
C 655	10.2	46.4	39	6	AR099751	AR099751 Sequence	C 728	10	45.5	25	6	AR034944	AR034944 Sequence
C 656	10.2	46.4	39	6	AR099751	AR099751 Sequence	C 729	10	45.5	25	6	AX196990	AX196990 Sequence
C 657	10.2	46.4	39	6	I06676	I06676 Sequence 13	C 730	10	45.5	25	6	AX196990	AX196990 Sequence
C 658	10.2	46.4	39	6	I06676	I06676 Sequence 13	C 731	10	45.5	25	6	AX448125	AX448125 Sequence
C 659	10.2	46.4	40	6	A66035	A66035 Sequence 17	C 732	10	45.5	25	6	AX448125	AX448125 Sequence
C 660	10.2	46.4	40	6	A66035	A66035 Sequence 17	C 733	10	45.5	25	6	I24207	I24207 Sequence 29
C 661	10.2	46.4	40	6	AR154825	AR154825 Sequence	C 734	10	45.5	25	6	I24207	I24207 Sequence 29
C 662	10.2	46.4	40	6	AR154825	AR154825 Sequence	C 735	10	45.5	25	6	I36774	I36774 Sequence 18
C 663	10.2	46.4	41	6	AX046598	AX046598 Sequence	C 736	10	45.5	25	6	I36774	I36774 Sequence 18
C 664	10.2	46.4	41	6	AX046598	AX046598 Sequence	C 737	10	45.5	26	6	AR063839	AR063839 Sequence
C 665	10.2	46.4	42	6	AX015114	AX015114 Sequence	C 738	10	45.5	26	6	AR063839	AR063839 Sequence
C 666	10.2	46.4	42	6	AX015114	AX015114 Sequence	C 739	10	45.5	27	6	AR187867	AR187867 Sequence
C 667	10.2	46.4	43	6	AR008303	AR008303 Sequence	C 740	10	45.5	27	6	AR187867	AR187867 Sequence
C 668	10.2	46.4	43	6	AR008303	AR008303 Sequence	C 741	10	45.5	27	6	AR190887	AR190887 Sequence
C 669	10.2	46.4	43	6	AR037293	AR037293 Sequence	C 742	10	45.5	27	6	AR190887	AR190887 Sequence
C 670	10.2	46.4	43	6	AR037293	AR037293 Sequence	C 743	10	45.5	27	6	AR196638	AR196638 Sequence
C 671	10.2	46.4	43	6	AR052163	AR052163 Sequence	C 744	10	45.5	27	6	AR196638	AR196638 Sequence
C 672	10.2	46.4	43	6	AR052163	AR052163 Sequence	C 745	10	45.5	27	6	I04705	I04705 Sequence 29
C 673	10.2	46.4	44	6	AR009627	AR009627 Sequence	C 746	10	45.5	27	6	I04705	I04705 Sequence 29
C 674	10.2	46.4	44	6	AR009627	AR009627 Sequence	C 747	10	45.5	27	6	I71983	I71983 Sequence 19
C 675	10.2	46.4	48	6	A41979	A41979 Sequence 20	C 748	10	45.5	27	6	I71983	I71983 Sequence 19
C 676	10.2	46.4	48	6	A41979	A41979 Sequence 20	C 749	10	45.5	27	6	I71984	I71984 Sequence 20
C 677	10.2	46.4	48	6	AX221492	AX221492 Sequence	C 750	10	45.5	27	6	I71984	I71984 Sequence 20
C 678	10.2	46.4	48	6	AX221492	AX221492 Sequence	C 751	10	45.5	27	6	I71986	I71986 Sequence 22
C 679	10.2	46.4	50	6	AR032974	AR032974 Sequence	C 752	10	45.5	27	6	I71986	I71986 Sequence 22
C 680	10.2	46.4	50	6	AR032974	AR032974 Sequence	C 753	10	45.5	27	6	I71986	I71986 Sequence 22
C 681	10.2	46.4	50	6	AR209638	AR209638 Sequence	C 754	10	45.5	27	10	MUSTCGXBQ	M5561 Mouse T-cell
C 682	10.2	46.4	50	6	AR209638	AR209638 Sequence	C 755	10	45.5	28	6	MUSTCGXBQ	M5561 Mouse T-cell
C 683	10.2	46.4	50	6	AX395202	AX395202 Sequence	C 756	10	45.5	28	6	A64577	A64577 Sequence 4
C 684	10.2	46.4	50	6	AX395202	AX395202 Sequence	C 757	10	45.5	29	6	AR133240	AR133240 Sequence
C 685	10.2	46.4	50	6	I29714	I29714 Sequence 58	C 758	10	45.5	29	6	AR143240	AR143240 Sequence
C 686	10.2	46.4	50	6	I29714	I29714 Sequence 58	C 759	10	45.5	30	6	A87158	A87158 Sequence 18
C 687	10.2	46.4	50	6	I91388	I91388 Sequence 58	C 760	10	45.5	30	6	A87158	A87158 Sequence 18
C 688	10.2	46.4	50	6	I91388	I91388 Sequence 58	C 761	10	45.5	30	6	A92743	A92743 Sequence 15
C 689	10.2	46.4	50	10	MUSTLSRRE2	M55074 Mub cervico	C 762	10	45.5	30	6	A92743	A92743 Sequence 15
C 690	10.2	46.4	50	10	MUSTLSRRE2	M55074 Mub cervico	C 763	10	45.5	30	6	AR182013	AR182013 Sequence
C 691	10.2	45.5	18	4	DOG2159P01	L78645 Canis famli	C 764	10	45.5	30	6	AR182013	AR182013 Sequence
C 692	10.2	45.5	18	4	DOG2159P01	L78645 Canis famli	C 765	10	45.5	30	6	AX033571	AX033571 Sequence
C 693	10.2	45.5	18	6	AR165361	AR165361 Sequence	C 766	10	45.5	30	6	AX033571	AX033571 Sequence
C 694	10.2	45.5	18	6	AR165361	AR165361 Sequence	C 767	10	45.5	30	6	AX297512	AX297512 Sequence
C 695	10.2	45.5	19	6	A83664	A83664 Sequence 7	C 768	10	45.5	30	6	AX297512	AX297512 Sequence
C 696	10.2	45.5	19	6	A83664	A83664 Sequence 7	C 769	10	45.5	31	6	A13741	A13741 Sequence
C 697	10.2	45.5	19	6	AR164414	AR164414 Sequence	C 770	10	45.5	31	6	A13741	A13741 Sequence
C 698	10.2	45.5	19	6	AR164414	AR164414 Sequence	C 771	10	45.5	31	6	A13742	A13742 Sequence
C 699	10.2	45.5	19	6	AX132423	AX132423 Sequence	C 772	10	45.5	31	6	A13742	A13742 Sequence
C 700	10.2	45.5	19	6	AX132423	AX132423 Sequence	C 773	10	45.5	31	6	A87140	A87140 Sequence 50
C 701	10.2	45.5	19	6	AX132424	AX132424 Sequence	C 774	10	45.5	31	6	A87140	A87140 Sequence 50
C 702	10.2	45.5	19	6	AX132424	AX132424 Sequence	C 775	10	45.5	31	6	A87183	A87183 Sequence 18
C 703	10.2	45.5	20	6	AX278432	AX278432 Sequence	C 776	10	45.5	31	6	A87183	A87183 Sequence 18
C 704	10.2	45.5	20	6	AX278432	AX278432 Sequence	C 777	10	45.5	31	6	AR195894	AR195894 Sequence
C 705	10.2	45.5	23	6	AR174973	AR174973 Sequence	C 778	10	45.5	31	6	AR195894	AR195894 Sequence
C 706	10.2	45.5	23	6	AR174973	AR174973 Sequence	C 779	10	45.5	31	6	AR206394	AR206394 Sequence
C 707	10.2	45.5	23	6	AR208529	AR208529 Sequence	C 780	10	45.5	31	6	AR206394	AR206394 Sequence
C 708	10.2	45.5	23	6	AR208529	AR208529 Sequence	C 781	10	45.5	31	6	BD002551	BD002551 Gene comp
C 709	10.2	45.5	23	6	AX212275	AX212275 Sequence	C 782	10	45.5	31	6	BD002551	BD002551 Gene comp
C 710	10.2	45.5	23	6	AX212275	AX212275 Sequence	C 783	10	45.5	31	6	BD002552	BD002552 Gene comp
C 711	10.2	45.5	24	6	AR084189	AR084189 Sequence	C 784	10	45.5	31	6	BD002552	BD002552 Gene comp
C 712	10.2	45.5	24	6	AR084189	AR084189 Sequence	C 785	10	45.5	32	6	AR029677	AR029677 Sequence
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C 716	10.2	45.5	24	6	AR208169	AR208169 Sequence	C 789	10	45.5	33	6	A36534	A36534 Sequence 75
C 717	10.2	45.5	24	6	AX007149	AX007149 Sequence	C 790	10	45.5	33	6	A36534	A36534 Sequence 75
C 718	10.2	45.5	24	6	AX007149	AX007149 Sequence	C 791	10	45.5	33	6	AR080157	AR080157 Sequence
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C 797	10	45.5	33	9	S80708	S80708 gamma delta	C 870	10	45.5	39	6	AR141025	AR141025 Sequence
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C 829	10	45.5	36	9	HUMTCGDCG	HUMTCGDCG	C 902	10	45.5	45	6	A13745	A13745 Oligonucleo
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C 832	10	45.5	37	6	A18680	A18680 Oligonucleo	C 905	10	45.5	47	6	A16640	A16640 Nucleotide
C 833	10	45.5	37	6	AR183322	AR183322 Sequence	C 906	10	45.5	47	6	A16640	A16640 Nucleotide
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C 850	10	45.5	38	6	AX222657	AX222657 Sequence	C 923	10	45.5	14	6	I06039	I06039 Sequence 8
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C 860	10	45.5	38	6	AX423982	AX423982 Sequence	C 933	10	44.5	20	6	A92150	A92150 Sequence 16
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ALIGNMENTS

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RESULT 1
LOCUS AX295560 20 bp DNA
DEFINITION Sequence 7322 from Patent WO0179548.
ACCESSION AX295560
VERSION AX295560.1 GI:17057249
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.

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REFERENCE
AUTHORS Barany, F., Zivri, M., Gerry, N.P., Favis, R. and Kliman, R.
TITLE Method of designing addressable array for detection of nucleic acid
JOURNAL
FEATURES
source
1. 20
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Hypothetical Probe Sequence"
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ORIGIN
Query Match 60.9%; Score 13.4; DB 6; Length 20;
Best Local Similarity 93.3%; Pred. No. 1.6e+05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
8 CGATATCGTCTCAG 22
5 CCAATATCGTCTCAG 19

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RESULT 2
LOCUS AX295560/c 20 bp DNA
DEFINITION Sequence 7322 from Patent WO0179548.
ACCESSION AX295560
VERSION AX295560.1 GI:17057249
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE
AUTHORS Barany, F., Zivri, M., Gerry, N.P., Favis, R. and Kliman, R.
TITLE Method of designing addressable array for detection of nucleic acid
JOURNAL CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES
source
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/db_xref="taxon:32630"
/note="Hypothetical Probe Sequence"
BASE COUNT 3 a 7 c 5 g 5 t
ORIGIN
Query Match 60.9%; Score 13.4; DB 6; Length 20;
Best Local Similarity 93.3%; Pred. No. 1.6e+05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
1 CTGAGACCGATATCG 15
19 CTGAGACCGATATCG 5

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RESULT 3
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DEFINITION Sequence 2689 from Patent WO0179548.
ACCESSION AX290927
VERSION AX290927.1 GI:17052610
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE
AUTHORS Barany, F., Zivri, M., Gerry, N.P., Favis, R. and Kliman, R.
TITLE Method of designing addressable array for detection of nucleic acid
JOURNAL CORNELL RESEARCH FOUNDATION, INC. (US)

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/db xref="taxon:32630"
/note="Hypothetical Probe Sequence"

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Best Local Similarity 93.3%; Pred. No. 1.6e+05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CGATATCGGTCTCAG 22
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| | | | | | | | | |
Db 5 CCATATCGGTCTCAG 19

RESULT 4
AX290927/c AX290927 24 bp DNA linear PAT 21-NOV-2001
LOCUS Sequence 2689 from Patent WO0179548.
DEFINITION AX290927
ACCESSION AX290927
VERSION AX290927.1 GI:117052610
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Barany, F., Zivvi, M., Gerry, N.P., Favis, R. and Kliman, R.
TITLE Method of designing addressable array for detection of nucleic acid
JOURNAL sequence differences using ligase detection reaction
Patent: WO 0179548-A 2689 25-OCT-2001;
CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES Location/Qualifiers
source 1. .24
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/db xref="taxon:32630"
/note="Hypothetical Probe Sequence"

BASE COUNT 3 a 8 c 6 g 7 t
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Query Match 60.9%; Score 13.4; DB 6; Length 24;
Best Local Similarity 93.3%; Pred. No. 1.6e+05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGAGACCGATATCG 15
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Db 19 CTGAGACCGATATCG 5

RESULT 5
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LOCUS Sequence 391 from patent US 6255458.
DEFINITION AR161400
ACCESSION AR161400
VERSION AR161400.1 GI:16227272
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 44)
AUTHORS Lomborg, N. and Kay, R.M.
TITLE High affinity human antibodies and human antibodies against digoxin
JOURNAL Patent: US 6255458-A 391 03-JUL-2001;
FEATURES Location/Qualifiers
source 1. .44
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RESULT 6
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LOCUS Sequence 391 from patent US 6255458.
DEFINITION AR161400
ACCESSION AR161400
VERSION AR161400.1 GI:16227272
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 44)
AUTHORS Lomborg, N. and Kay, R.M.
TITLE High affinity human antibodies and human antibodies against digoxin
JOURNAL Patent: US 6255458-A 391 03-JUL-2001;
FEATURES Location/Qualifiers
source 1. .44
/organism="unknown"

BASE COUNT 10 a 11 c 12 g 11 t
ORIGIN

Query Match 59.1%; Score 13; DB 6; Length 44;
Best Local Similarity 76.2%; Pred. No. 2.3e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CTGAGACCGATATCGGTCTCA 21
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Db 29 CTGGGACAGATTTCACCTCA 9

RESULT 7
AX292255 AX292255 24 bp DNA linear PAT 21-NOV-2001
LOCUS Sequence 4017 from Patent WO0179548.
DEFINITION AX292255
ACCESSION AX292255
VERSION AX292255.1 GI:117053938
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Barany, F., Zivvi, M., Gerry, N.P., Favis, R. and Kliman, R.
TITLE Method of designing addressable array for detection of nucleic acid
JOURNAL sequence differences using ligase detection reaction
Patent: WO 0179548-A 4017 25-OCT-2001;
CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES Location/Qualifiers
source 1. .24
/organism="synthetic construct"
/db xref="taxon:32630"
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Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Db 6 CTGGGACCGATATCGGTCT 24

RESULT 8
AX292255/c AX292255 24 bp DNA linear PAT 21-NOV-2001
LOCUS Sequence 4017 from Patent WO0179548.
DEFINITION AX292255
ACCESSION AX292255

VERSION AX292255.1 GI:17053938
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM synthetic construct.
 REFERENCE 1
 AUTHORS Barany, F., Zivri, M., Gerry, N.P., Favis, R. and Kliman, R.
 TITLE Method of designing addressable array for detection of nucleic acid
 JOURNAL sequence difference using ligase detection reaction
 PATENT: WO 0179548-A 4017 25-OCT-2001;
 CORNELL RESEARCH FOUNDATION, INC. (US)
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 /db_xref="taxon:32630"
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 Query Match 57.3%; Score 12.6; DB 6; Length 24;
 Best Local Similarity 78.9%; Pred. No. 3.8e+05;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 4 AGACCGATATCGGTCTCAG 22
 24 AGACCGGTATGGGTCCAG 6
 Db
 RESULT 9
 AX189358 25 bp DNA linear PAT 08-AUG-2001
 LOCUS Sequence 15 from Patent WO0148244.
 DEFINITION AX189358
 ACCESSION AX189358
 VERSION AX189358.1 GI:15142870
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM synthetic construct.
 REFERENCE 1 (bases 1 to 25)
 AUTHORS Casey, W.M., Chen, J.G., Colton, H.M., Taylor, D.G. and Weiner, M.P.
 TITLE Detection of single nucleotide polymorphisms
 JOURNAL Patent: WO 0148244-A 15 05-JUL-2001;
 GLAXO GROUP LIMITED (GB)
 FEATURES
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 /db_xref="taxon:32630"
 BASE COUNT 5 a 8 c 9 g 3 t
 ORIGIN
 Query Match 57.3%; Score 12.6; DB 6; Length 25;
 Best Local Similarity 78.9%; Pred. No. 3.8e+05;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 3 GAGACCGATATCGGTCTCA 21
 5 GATACCGATCTCGGCGCCA 23
 Db
 RESULT 10
 AX189358 25 bp DNA linear PAT 08-AUG-2001
 LOCUS Sequence 15 from Patent WO0148244.
 DEFINITION AX189358
 ACCESSION AX189358
 VERSION AX189358.1 GI:15142870
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM synthetic construct.
 REFERENCE 1 (bases 1 to 25)
 AUTHORS Casey, W.M., Chen, J.G., Colton, H.M., Taylor, D.G. and Weiner, M.P.
 TITLE Detection of single nucleotide polymorphisms
 JOURNAL Patent: WO 0148244-A 15 05-JUL-2001;

GLAXO GROUP LIMITED (GB)
 FEATURES
 source 1. .25
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 BASE COUNT 5 a 8 c 9 g 3 t
 ORIGIN
 Query Match 57.3%; Score 12.6; DB 6; Length 25;
 Best Local Similarity 78.9%; Pred. No. 3.8e+05;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 2 TGAGACCGATATCGGTCTC 20
 23 TGGCGCCGAGATCGGTATC 5
 Db
 RESULT 11
 BD009441 21 bp DNA linear PAT 31-JAN-2002
 LOCUS Probes, methods and kits for detection and typing of Helicobacter
 DEFINITION pylori, nucleic acids in biological samples.
 ACCESSION BD009441 GI:18637814
 VERSION BD009441.1 GI:18637814
 KEYWORDS JP 2001502536-A/33.
 SOURCE unidentified.
 ORGANISM unidentified.
 REFERENCE 1 (bases 1 to 21)
 AUTHORS Quint, W. and Doorn, L.J.V.
 TITLE Probes, methods and kits for detection and typing of Helicobacter
 JOURNAL pylori, nucleic acids in biological samples
 PATENT: JP 2001502536-A 33 27-FEB-2001;
 INNOGENETICS NV, DDL BV
 COMMENT OS Unidentified.
 PN JP 2001502536-A/33
 PD 27-FEB-2001
 PF 10-OCT-1997 JP 1998518004
 PR 16-OCT-1996 EP 96870131.8
 PI WILHELMUS QUINT, LEENDERT JAN VAN DOORN
 PC C12Q1/68, C07K14/205, C12N15/11
 CC CC
 FH Key
 FT source 1. .21
 Location/Qualifiers
 FEATURES
 source 1. .21
 /organism="Unidentified".
 Location/Qualifiers
 BASE COUNT 9 a 3 c 5 g 2 t 2 others
 ORIGIN
 Query Match 56.4%; Score 12.4; DB 6; Length 21;
 Best Local Similarity 72.2%; Pred. No. 4.8e+05;
 Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 4 AGACCGATATCGGTCTCA 21
 1 AGACCGATAAGGKCTTA 18
 Db
 RESULT 12
 BD009441 21 bp DNA linear PAT 31-JAN-2002
 LOCUS Probes, methods and kits for detection and typing of Helicobacter
 DEFINITION pylori, nucleic acids in biological samples.
 ACCESSION BD009441
 VERSION BD009441.1 GI:18637814
 KEYWORDS JP 2001502536-A/33.
 SOURCE unidentified.
 ORGANISM unidentified.
 REFERENCE 1 (bases 1 to 21)

AUTHORS Quint, W. and Doorn, L.J.V.
TITLE Probes, methods and kits for detection and typing of Helicobacter
JOURNAL pylori nucleic acids in biological samples
COMMENT Patent: JP 2001502536-A 33 27-FEB-2001;
INNOGENETICS NV, DDL BV
OS Unidentified
PN JP 2001502536-A/33
PD 27-FEB-2001
PF 10-OCT-1997 JP 1998518004
PR 16-OCT-1996 EP 96870131.8
PI WILHELMUS QUINT, LEENDERT JAN VAN DOORN
PC C12Q1/68, C07K14/205, C12N15/11
CC
FH
FT
FT
Key Location/Qualifiers
source /organism='Unidentified'.
Location/Qualifiers
1. .21
/organism='unidentified'
/db_xref='taxon:32644'
BASE COUNT 9 a 3 c 5 g 2 t 2 others
ORIGIN
Query Match 56.4%; Score 12.4; DB 6; Length 21;
Best Local Similarity 72.2%; Pred. No. 4.8e+05;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 2 TGAGACCGATATCGGTCT 19
Db 18 TTAGMCCRTATCGGTCT 1
RESULT 13
LOCUS 127040 30 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 61 from patent US 5563036.
ACCESSION 127040
VERSION 127040.1 GI:1817816
KEYWORDS
SOURCE Unknown.
ORGANISM Unidentified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Peterson, M.G., Baichwal, V.R. and Strulovici, B.
TITLE Transcription factor-DNA binding assay
JOURNAL Patent: US 5563036-A 61 08-OCT-1996;
FEATURES Location/Qualifiers
source 1. .30
/organism='unknown'
BASE COUNT 9 a 7 c 9 g 5 t
ORIGIN
Query Match 56.4%; Score 12.4; DB 6; Length 30;
Best Local Similarity 72.7%; Pred. No. 4.6e+05;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 CTGAGACCGATATCGGTCTCAG 22
Db 5 CTGATCCGAAACGGTACCAG 26
RESULT 14
LOCUS 127040/c 30 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 61 from patent US 5563036.
ACCESSION 127040
VERSION 127040.1 GI:1817816
KEYWORDS
SOURCE Unknown.
ORGANISM Unidentified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Peterson, M.G., Baichwal, V.R. and Strulovici, B.

TITLE Transcription factor-DNA binding assay
JOURNAL Patent: US 5563036-A 61 08-OCT-1996;
FEATURES Location/Qualifiers
source 1. .30
/organism='unknown'
BASE COUNT 9 a 7 c 9 g 5 t
ORIGIN
Query Match 56.4%; Score 12.4; DB 6; Length 30;
Best Local Similarity 72.7%; Pred. No. 4.6e+05;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 CTGAGACCGATATCGGTCTCAG 22
Db 26 CTGATCCGTTTTCGTACCAG 5
RESULT 15
LOCUS A41699 32 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 26 from Patent EP0630968.
ACCESSION A41699
VERSION A41699.1 GI:2297322
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 32)
AUTHORS Fritz, H., Hennecke, F. and Kolmar, H.
TITLE Genetic selection of proteins able to bind a ligand by
JOURNAL signal-transduction in a microorganism
COMMENT Patent: EP 0630968-A 26 28-DEC-1994;
BEHRINGERwerke AG (DE)
Other publication JP 6343472 941220
Other publication AU 6461494 941215
Other publication CA 2125536 941211
Other publication DE 4319296 941215.
FEATURES Location/Qualifiers
source 1. .32
/organism='unidentified'
/db_xref='taxon:32644'
BASE COUNT 7 a 12 c 5 g 8 t
ORIGIN
Query Match 56.4%; Score 12.4; DB 6; Length 32;
Best Local Similarity 92.9%; Pred. No. 4.5e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 8 CGATATCGGTCTCA 21
Db 9 CGATATCGGTCTCA 22
RESULT 16
LOCUS A41699 32 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 26 from Patent EP0630968.
ACCESSION A41699
VERSION A41699.1 GI:2297322
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 32)
AUTHORS Fritz, H., Hennecke, F. and Kolmar, H.
TITLE Genetic selection of proteins able to bind a ligand by
JOURNAL signal-transduction in a microorganism
COMMENT Patent: EP 0630968-A 26 28-DEC-1994;
BEHRINGERwerke AG (DE)
Other publication JP 6343472 941220
Other publication AU 6461494 941215
Other publication CA 2125536 941211
Other publication DE 4319296 941215.

FEATURES
source 1..32 Location/Qualifiers
/db_xref="taxon:32644"
BASE COUNT 7 a 12 c 5 g 8 t
ORIGIN

Query Match 56.4%; Score 12.4; DB 6; Length 32;
Best Local Similarity 92.9%; Pred. No. 4.5e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGAGACCGATATCG 15
Db 22 TGAGAACGATATCG 9

RESULT 17
AX361282 45 bp DNA linear PAT 15-FEB-2002
LOCUS AX361282 Sequence 13 from Patent WO0208435.
DEFINITION AX361282
ACCESSION AX361282
VERSION AX361282.1 GI:18693905
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 Ertl, P.F., Gough, G.W. and Ring, C.J.
AUTHORS Codon-optimized papilloma virus sequences
TITLE Patent: WO 0208435-A 13 31-JAN-2002;
JOURNAL GLAXO GROUP LIMITED (GB)
FEATURES Location/Qualifiers
source 1..45
/db_xref="taxon:32630"
/note="Oligonucleotide linker"
BASE COUNT 8 a 15 c 14 g 8 t
ORIGIN

Query Match 56.4%; Score 12.4; DB 6; Length 45;
Best Local Similarity 72.7%; Pred. No. 4.3e+05;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CTGAGACCGATATCGGTCAG 22
Db 19 CTGCTACCGATATCGCTACGCG 40

RESULT 18
AX361282 45 bp DNA linear PAT 15-FEB-2002
LOCUS AX361282 Sequence 13 from Patent WO0208435.
DEFINITION AX361282
ACCESSION AX361282
VERSION AX361282.1 GI:18693905
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 Ertl, P.F., Gough, G.W. and Ring, C.J.
AUTHORS Codon-optimized papilloma virus sequences
TITLE Patent: WO 0208435-A 13 31-JAN-2002;
JOURNAL GLAXO GROUP LIMITED (GB)
FEATURES Location/Qualifiers
source 1..45
/db_xref="taxon:32630"
/note="Oligonucleotide linker"
BASE COUNT 8 a 15 c 14 g 8 t
ORIGIN

Query Match 56.4%; Score 12.4; DB 6; Length 45;
Best Local Similarity 72.7%; Pred. No. 4.3e+05;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CTGAGACCGATATCGGTCAG 22
Db 40 CCGCTACCGATATCGGTACG 19

RESULT 19
AX047302 24 bp DNA linear PAT 15-DEC-2000
LOCUS AX047302 Sequence 16 from Patent WO0068374.
DEFINITION AX047302
ACCESSION AX047302
VERSION AX047302.1 GI:11876573
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 Heifetz, P.B., Patton, D.A., Levin, J.Z., Que, Q., de Haan, P.T. and
AUTHORS Heifetz, P.B., Patton, D.A., Levin, J.Z., Que, Q., de Haan, P.T. and
TITLE Regulation of viral gene expression
JOURNAL Patent: WO 0068374-A 16 16-NOV-2000;
Novartis AG (CH); Novartis-Erfindungen Verwaltungsgesellschaft
m.b.H. (AT)
FEATURES Location/Qualifiers
source 1..24
/db_xref="taxon:32630"
/note="HINK284"
BASE COUNT 7 a 7 c 4 g 6 t
ORIGIN

Query Match 55.5%; Score 12.2; DB 6; Length 24;
Best Local Similarity 82.4%; Pred. No. 5.8e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 ACCGATATCGGTCAG 22
Db 5 AACGAATCGGTCAG 21

RESULT 20
AX047302 24 bp DNA linear PAT 15-DEC-2000
LOCUS AX047302 Sequence 16 from Patent WO0068374.
DEFINITION AX047302
ACCESSION AX047302
VERSION AX047302.1 GI:11876573
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 Heifetz, P.B., Patton, D.A., Levin, J.Z., Que, Q., de Haan, P.T. and
AUTHORS Heifetz, P.B., Patton, D.A., Levin, J.Z., Que, Q., de Haan, P.T. and
TITLE Regulation of viral gene expression
JOURNAL Patent: WO 0068374-A 16 16-NOV-2000;
Novartis AG (CH); Novartis-Erfindungen Verwaltungsgesellschaft
m.b.H. (AT)
FEATURES Location/Qualifiers
source 1..24
/db_xref="taxon:32630"
/note="HINK284"
BASE COUNT 7 a 7 c 4 g 6 t
ORIGIN

Query Match 55.5%; Score 12.2; DB 6; Length 24;
Best Local Similarity 82.4%; Pred. No. 5.8e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGAGACCGATATCGGT 17
Db 21 CTGAGACCGAATTCGTT 5

RESULT 21
E06104
LOCUS
DEFINITION Oligonucleotide specific to subtype Pt of Hepatitis C virus.
ACCESSION E06104
VERSION E06104.1 GI:2174291
KEYWORDS JP 199337000-A/28.
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 26)
AUTHORS Chayama,K. and Kumada,H.
TITLE METHOD FOR EXAMINING C TYPE HEPATITIS VIRUS AND PRIMER SET USED FOR THE SAME
JOURNAL Patent: JP 199337000-A 28 21-DEC-1993;
CHAYAMA KAZUAKI
COMMENT OS Artificial gene
OC Artificial sequence; Genes.
OS Hepatitis C virus
PN JP 199337000-A/28
PD 21-DEC-1993
PF 04-JUN-1992 JP 1992168226
PI CHAYAMA KAZUAKI, KUMADA HIROMITSU
PC C12Q1/68, C12N15/10, C12N15/11, C12Q1/70;
CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
FEATURES
source 1..26
Location/Qualifiers
/db_xref="synthetic construct"
/db_xref="taxon:32630" 4 t
BASE COUNT 7 a 8 c 7 g 4 t
ORIGIN
Query Match 55.5%; Score 12.2; DB 6; Length 26;
Best Local Similarity 82.4%; Pred. No. 5.8e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CTGAGACCGATATCGGT 17
|||||
7 CTGAGAGCGACATCCGT 23
Db
RESULT 22
E06104
LOCUS
DEFINITION Oligonucleotide specific to subtype Pt of Hepatitis C virus.
ACCESSION E06104
VERSION E06104.1 GI:2174291
KEYWORDS JP 199337000-A/28.
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 26)
AUTHORS Chayama,K. and Kumada,H.
TITLE METHOD FOR EXAMINING C TYPE HEPATITIS VIRUS AND PRIMER SET USED FOR THE SAME
JOURNAL Patent: JP 199337000-A 28 21-DEC-1993;
CHAYAMA KAZUAKI
COMMENT OS Artificial gene
OC Artificial sequence; Genes.
OS Hepatitis C virus
PN JP 199337000-A/28
PD 21-DEC-1993
PF 04-JUN-1992 JP 1992168226
PI CHAYAMA KAZUAKI, KUMADA HIROMITSU
PC C12Q1/68, C12N15/10, C12N15/11, C12Q1/70;
CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
FEATURES
source 1..26
Location/Qualifiers
/db_xref="synthetic construct"
/db_xref="taxon:32630" 4 t
BASE COUNT 7 a 8 c 7 g 4 t
ORIGIN
Query Match 55.5%; Score 12.2; DB 6; Length 26;
Best Local Similarity 82.4%; Pred. No. 5.8e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CTGAGACCGATATCGGT 17
|||||
7 CTGAGAGCGACATCCGT 23
Db
RESULT 23
E06104
LOCUS
DEFINITION PCR primer for detecting Hepatitis C virus.
ACCESSION E10842
VERSION E10842.1 GI:22027936
KEYWORDS JP 199605672-A/4.
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 26)
AUTHORS Chayama,K. and Kumada,H.
TITLE GENE OF TYPE C HEPATITIS VIRUS
JOURNAL Patent: JP 199605672-A 4 05-MAR-1996;
CHAYAMA KAZUAKI
COMMENT OS None
OC Artificial sequences.
PN JP 199605672-A/4
PD 05-MAR-1996
PF 26-AUG-1994 JP 1994223933
PI CHAYAMA KAZUAKI, KUMADA HIROMITSU
PC C12N15/09, A61K39/29, C07K14/18, C12N1/21, C12P21/02, C12Q1/68, PC G01N33/576,
PC (C12N1/21, C12R1:91), (C12P21/02, C12R1:91);
CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
FH Key
FT Location/Qualifiers
source 1..26
Location/Qualifiers
/db_xref="taxon:32644" 4 t
BASE COUNT 7 a 8 c 7 g 4 t
ORIGIN
Query Match 55.5%; Score 12.2; DB 6; Length 26;
Best Local Similarity 82.4%; Pred. No. 5.8e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CTGAGACCGATATCGGT 17
|||||
7 CTGAGAGCGACATCCGT 23
Db
RESULT 24
E10842
LOCUS
DEFINITION PCR primer for detecting Hepatitis C virus.
ACCESSION E10842
VERSION E10842.1 GI:22027936
KEYWORDS JP 199605672-A/4.
SOURCE unidentified.

FEATURES
CC anti-sense: No.
Location/Qualifiers
source 1..26
/db_xref="synthetic construct"
/db_xref="taxon:32630" 4 t
BASE COUNT 7 a 8 c 7 g 4 t
ORIGIN
Query Match 55.5%; Score 12.2; DB 6; Length 26;
Best Local Similarity 82.4%; Pred. No. 5.8e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 6 ACCGATATCGTCTCAG 22
|||||
23 ACCGATGCTGCTCTCAG 7
Db
RESULT 23
E10842
LOCUS
DEFINITION PCR primer for detecting Hepatitis C virus.
ACCESSION E10842
VERSION E10842.1 GI:22027936
KEYWORDS JP 199605672-A/4.
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 26)
AUTHORS Chayama,K. and Kumada,H.
TITLE GENE OF TYPE C HEPATITIS VIRUS
JOURNAL Patent: JP 199605672-A 4 05-MAR-1996;
CHAYAMA KAZUAKI
COMMENT OS None
OC Artificial sequences.
PN JP 199605672-A/4
PD 05-MAR-1996
PF 26-AUG-1994 JP 1994223933
PI CHAYAMA KAZUAKI, KUMADA HIROMITSU
PC C12N15/09, A61K39/29, C07K14/18, C12N1/21, C12P21/02, C12Q1/68, PC G01N33/576,
PC (C12N1/21, C12R1:91), (C12P21/02, C12R1:91);
CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
FH Key
FT Location/Qualifiers
source 1..26
Location/Qualifiers
/db_xref="taxon:32644" 4 t
BASE COUNT 7 a 8 c 7 g 4 t
ORIGIN
Query Match 55.5%; Score 12.2; DB 6; Length 26;
Best Local Similarity 82.4%; Pred. No. 5.8e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CTGAGACCGATATCGGT 17
|||||
7 CTGAGAGCGACATCCGT 23
Db
RESULT 24
E10842
LOCUS
DEFINITION PCR primer for detecting Hepatitis C virus.
ACCESSION E10842
VERSION E10842.1 GI:22027936
KEYWORDS JP 199605672-A/4.
SOURCE unidentified.

ORGANISM unidentified
REFERENCE 1 (bases 1 to 26)
AUTHORS Chayama, K. and Kumada, H.
TITLE GENE OF TYPE C HEPATITIS VIRUS
JOURNAL Patent: JP 196056672-A 4 05-MAR-1996;
CHAYAMA KAZUAKI
COMMENT OS None
OC Artificial sequences.
PN JP 196056672-A/4
PD 05-MAR-1996
PF 26-AUG-1994 JP 1994223933
PI CHAYAMA KAZUAKI, KUMADA HIROMITSU
PC C12N15/09, A61K39/29, C07K14/18, C12N1/21, C12P21/02, C12Q1/68, PC
G01N33/576
PC (C12N1/21, C12R1/91), (C12P21/02, C12R1/91);
CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
FH Key Location/Qualifiers
FT source 1..26
Location/Qualifiers
1..26 /organism='Artificial sequences'
/db_xref='taxon:32644'
BASE COUNT 7 a 8 c 7 g 4 t
ORIGIN
Query Match 55.5%; Score 12.2; DB 6; Length 26;
Best Local Similarity 82.4%; Pred. No. 5.6e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 6 ACCGATATCGGTCTCAG 22
DB 23 ACCGATGTCTGCTCAG 7
RESULT 25
LOCUS AR120578 33 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 8 from patent US 6159477.
ACCESSION AR120578
VERSION AR120578.1 GI:14104154
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 33)
AUTHORS Audonnet, J.-C. and Baudu, P.
TITLE Canine herpesvirus based recombinant live vaccine, in particular
JOURNAL against canine distemper, rabies or the parainfluenza 2 virus
PATENT: US 6159477-A 8 12-DEC-2000;
FEATURES Location/Qualifiers
source 1..33
/organism='unknown'
BASE COUNT 8 a 9 c 10 g 6 t
ORIGIN
Query Match 55.5%; Score 12.2; DB 6; Length 33;
Best Local Similarity 82.4%; Pred. No. 5.6e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 5 GACCGATATCGGTCTCA 21
DB 17 GATCGATATCGGCCCA 33
RESULT 26
LOCUS AR120578 33 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 8 from patent US 6159477.
ACCESSION AR120578
VERSION AR120578.1 GI:14104154
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 33)
AUTHORS Audonnet, J.-C. and Baudu, P.
TITLE Canine herpesvirus based recombinant live vaccine, in particular
JOURNAL against canine distemper, rabies or the parainfluenza 2 virus
PATENT: US 6159477-A 9 12-DEC-2000;
FEATURES Location/Qualifiers

DEFINITION Sequence 8 from patent US 6159477.
ACCESSION AR120578
VERSION AR120578.1 GI:14104154
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 33)
AUTHORS Audonnet, J.-C. and Baudu, P.
TITLE Canine herpesvirus based recombinant live vaccine, in particular
JOURNAL against canine distemper, rabies or the parainfluenza 2 virus
PATENT: US 6159477-A 8 12-DEC-2000;
FEATURES Location/Qualifiers
source 1..33
/organism='unknown'
BASE COUNT 8 a 9 c 10 g 6 t
ORIGIN
Query Match 55.5%; Score 12.2; DB 6; Length 33;
Best Local Similarity 82.4%; Pred. No. 5.6e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 TGAGACCGATATCGGTC 18
DB 33 TGAGCCCGATATCGATC 17
RESULT 27
LOCUS AR120579 33 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 9 from patent US 6159477.
ACCESSION AR120579
VERSION AR120579.1 GI:14104155
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 33)
AUTHORS Audonnet, J.-C. and Baudu, P.
TITLE Canine herpesvirus based recombinant live vaccine, in particular
JOURNAL against canine distemper, rabies or the parainfluenza 2 virus
PATENT: US 6159477-A 9 12-DEC-2000;
FEATURES Location/Qualifiers
source 1..33
/organism='unknown'
BASE COUNT 6 a 10 c 9 g 8 t
ORIGIN
Query Match 55.5%; Score 12.2; DB 6; Length 33;
Best Local Similarity 82.4%; Pred. No. 5.6e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 TGAGACCGATATCGGTC 18
DB 5 TGAGCCCGATATCGATC 21
RESULT 28
LOCUS AR120579 33 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 9 from patent US 6159477.
ACCESSION AR120579
VERSION AR120579.1 GI:14104155
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 33)
AUTHORS Audonnet, J.-C. and Baudu, P.
TITLE Canine herpesvirus based recombinant live vaccine, in particular
JOURNAL against canine distemper, rabies or the parainfluenza 2 virus
PATENT: US 6159477-A 9 12-DEC-2000;
FEATURES Location/Qualifiers

source 1..33
/organism="unknown"
BASE COUNT 6 a 10 c 9 g 8 t
ORIGIN

Query Match 55.5%; Score 12.2; DB 6; Length 33;
Best Local Similarity 82.4%; Pred. No. 5.6e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 GACCGATATCGGCTCA 21
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Db 21 GATCGATATCGGCTCA 5

RESULT 29
LOCUS 173498 33 bp DNA linear PAT 03-APR-1998
DEFINITION Sequence 1 from patent US 5686579.
ACCESSION 173498
VERSION 173498.1 GI:3009639
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE 1 (bases 1 to 33)
AUTHORS Sham, E.Y., Rothenstein, A. and Ramjessingh, M.
TITLE Use of antibody/antigen interactions to protect biologically active proteins and peptides
JOURNAL Patent: US 5686579-A 1 11-NOV-1997;
FEATURES
source 1..33
/organism="unknown"
BASE COUNT 6 a 9 c 6 g 5 t 7 others
ORIGIN

Query Match 55.5%; Score 12.2; DB 6; Length 33;
Best Local Similarity 70.6%; Pred. No. 5.6e+05;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 5 GACCGATATCGGCTCA 21
|||
Db 5 GACCGATATCGGCTCA 21

RESULT 30
LOCUS 173498 33 bp DNA linear PAT 03-APR-1998
DEFINITION Sequence 1 from patent US 5686579.
ACCESSION 173498
VERSION 173498.1 GI:3009639
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE 1 (bases 1 to 33)
AUTHORS Sham, E.Y., Rothenstein, A. and Ramjessingh, M.
TITLE Use of antibody/antigen interactions to protect biologically active proteins and peptides
JOURNAL Patent: US 5686579-A 1 11-NOV-1997;
FEATURES
source 1..33
/organism="unknown"
BASE COUNT 6 a 9 c 6 g 5 t 7 others
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Best Local Similarity 70.6%; Pred. No. 5.6e+05;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGAGACCGATATCGGTC 18
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Db 21 TVAGSACGATATCGGTC 5

RESULT 31
LOCUS AX099887 37 bp DNA linear PAT 02-APR-2001
DEFINITION Sequence 36 from Patent WO0120014.
ACCESSION AX099887
VERSION AX099887.1 GI:13538913
KEYWORDS
SOURCE synthetic construct.
ORGANISM
REFERENCE 1 (bases 1 to 37)
AUTHORS Schouten, G.J., Vogels, R. and Opstelten, D.J.
TITLE Modified adenoviral vectors for use in gene therapy
JOURNAL Patent: WO 0120014-A 36 22-MAR-2001;
FEATURES
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Best Local Similarity 82.4%; Pred. No. 5.5e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TGAGACCGATATCGGTC 18
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Db 17 TTAGACAGATATCGATC 1

RESULT 32
LOCUS AX099887 37 bp DNA linear PAT 02-APR-2001
DEFINITION Sequence 36 from Patent WO0120014.
ACCESSION AX099887
VERSION AX099887.1 GI:13538913
KEYWORDS
SOURCE synthetic construct.
ORGANISM
REFERENCE 1 (bases 1 to 37)
AUTHORS Schouten, G.J., Vogels, R. and Opstelten, D.J.
TITLE Modified adenoviral vectors for use in gene therapy
JOURNAL Patent: WO 0120014-A 36 22-MAR-2001;
FEATURES
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Location/Qualifiers
primer_bind 1..37
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Best Local Similarity 82.4%; Pred. No. 5.5e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 17 TTAGACAGATATCGATC 1

RESULT 33
LOCUS AX138008 37 bp DNA linear PAT 30-MAY-2001
DEFINITION Sequence 37 from Patent Epi083229.

ACCESSION AX138008
VERSION AX138008.1 GI:14274103
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ORGANISM synthetic construct.
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Best Local Similarity 82.4%; Pred. No. 5.5e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Db 1 GATCGATATCTGTCTAA 17
RESULT 34
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LOCUS AX138008 37 bp. DNA linear PAT 30-MAY-2001
DEFINITION Sequence 37 from Patent EP1083229.
ACCESSION AX138008
VERSION AX138008.1 GI:14274103
KEYWORDS
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ORGANISM synthetic construct.
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Query Match 55.5%; Score 12.2; DB 6; Length 37;
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Db 17 TTGACGATATCGATC 1
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LOCUS ARI20598 39 bp. DNA linear PAT 16-MAY-2001
DEFINITION Sequence 28 from patent US 6159477.
ACCESSION ARI20598
VERSION ARI20598.1 GI:14104174
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
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Best Local Similarity 82.4%; Pred. No. 5.5e+05;
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Db 5 TGGGCGCGATATCGATC 21
RESULT 38
ARI20599/c

ORIGIN
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Best Local Similarity 82.4%; Pred. No. 5.5e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Db 23 GATCGATATCGGGCCCA 39
RESULT 36
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LOCUS ARI20598 39 bp. DNA linear PAT 16-MAY-2001
DEFINITION Sequence 28 from patent US 6159477.
ACCESSION ARI20598
VERSION ARI20598.1 GI:14104174
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
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/organism="unknown"
BASE COUNT 9 a 11 c 12 g 7 t
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Best Local Similarity 82.4%; Pred. No. 5.5e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 TGAGACCGATATCGGTC 18
Db 39 TGGGCGCGATATCGATC 23
RESULT 37
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LOCUS ARI20599 39 bp. DNA linear PAT 16-MAY-2001
DEFINITION Sequence 29 from patent US 6159477.
ACCESSION ARI20599
VERSION ARI20599.1 GI:14104175
KEYWORDS
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ORGANISM Unknown.
FEATURES
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BASE COUNT 7 a 12 c 11 g 9 t
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Best Local Similarity 82.4%; Pred. No. 5.5e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 TGAGACCGATATCGGTC 18
Db 5 TGGGCGCGATATCGATC 21
RESULT 38
ARI20599/c

LOCUS AR120599 39 bp DNA linear PAT 16-MAY-2001
 DEFINITION Sequence 29 from patent US 6159477.
 ACCESSION AR120599
 VERSION AR120599.1 GI:14104175
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 39)
 AUTHORS Audonnet,J.-C. and Baudu,P.
 TITLE Canine herpesvirus based recombinant live vaccine, in particular
 against canine distemper, rabies or the parainfluenza 2 virus
 JOURNAL Patent: US 6159477-A 29 12-DEC-2000;
 FEATURES
 source Location/Qualifiers
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 BASE COUNT 7 a 12 c 11 g 9 t
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Query Match 55.5%; Score 12.2; DB 6; Length 39;
 Best Local Similarity 82.4%; Pred. No. 5.5e+05;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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 DB 21 GATCGATATCGGCGCCA 5

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 DEFINITION 127047
 ACCESSION 127047
 VERSION 127047.1 GI:1817823
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 28)
 AUTHORS Peterson,M.G., Baichwal,V.R. and Strulovici,B.
 TITLE Transcription factor-DNA binding assay
 JOURNAL Patent: US 5563036-A 68 08-OCT-1996;
 FEATURES
 source Location/Qualifiers
 1..28
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 BASE COUNT 9 a 7 c 9 g 3 t
 ORIGIN

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OY 3 GAGACCGATATCGGTCTCAG 22
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 DB 6 GTGACCGAAACCGTGTGAG 25

RESULT 40
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 LOCUS Sequence 68 from patent US 5563036.
 DEFINITION 127047
 ACCESSION 127047
 VERSION 127047.1 GI:1817823
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 28)
 AUTHORS Peterson,M.G., Baichwal,V.R. and Strulovici,B.
 TITLE Transcription factor-DNA binding assay
 JOURNAL Patent: US 5563036-A 68 08-OCT-1996;
 FEATURES
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BASE COUNT 9 a 7 c 9 g 3 t
 ORIGIN /organism="unknown"

Query Match 54.5%; Score 12; DB 6; Length 28;
 Best Local Similarity 75.0%; Pred. No. 7.1e+05;
 Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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 DB 25 CTCACACCGTTTTCGGTCA 6

Search completed: June 14, 2003, 22:14:56
 Job time : 1000 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 14, 2003, 09:41:20 ; Search time 208 Seconds
(without alignments)
238.192 Million cell updates/sec

Title: US-09-532-001-1
Perfect score: 22
Sequence: 1 CTGAGACCGATATCGGTCTCAG 22

Scoring table: IDENTITY_NTC
Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 112599159 residues
Total number of hits satisfying chosen parameters: 2166140

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	22	100.0	22	19	AAV70907	Antisense probe fo
2	22	100.0	22	19	AAV70907	Antisense probe fo
3	14.2	64.5	28	21	AAV70834	Molecular interact
4	14.2	64.5	28	21	AAV70834	Molecular interact
5	14	63.6	33	21	ABA98894	DNA sequence 2 rel
6	14	63.6	33	21	ABA98894	DNA sequence 2 rel
7	14	63.6	40	21	AA295872	Polynucleotide seq
8	14	63.6	40	21	AA295872	Polynucleotide seq
9	13.6	61.8	33	22	AAH46201	Hexapetaloid dupli

10	13.6	61.8	33	22	AAH46201	Hexapetaloid dupli
11	13.4	60.9	20	24	AB195602	Capture oligonucle
12	13.4	60.9	20	24	AB195602	Capture oligonucle
13	13.4	60.9	24	24	AB187774	Capture oligonucle
14	13.4	60.9	24	24	AB187774	Capture oligonucle
15	13.4	60.9	24	24	AB187775	Capture oligonucle
16	13.4	60.9	24	24	AB187775	Capture oligonucle
17	13	59.1	36	20	AAH04272	HAV-A linker regio
18	13	59.1	36	20	AAH04272	HAV-A linker regio
19	13	59.1	44	18	AAV78823	Kappa light chain
20	13	59.1	44	18	AAV78823	Kappa light chain
21	13	59.1	44	19	AAV39264	Primer o-561 used
22	13	59.1	44	19	AAV39264	Primer o-561 used
23	13	59.1	44	20	AAZ22018	Oligonucleotide us
24	13	59.1	44	20	AAZ22018	Oligonucleotide us
25	12.8	58.2	24	21	AAZ43102	PCR primer for C.
26	12.8	58.2	24	21	AAZ43102	PCR primer for C.
27	12.8	58.2	34	21	AAZ89641	Plasmid pUC19 prim
28	12.8	58.2	34	21	AAZ89641	Plasmid pUC19 prim
29	12.8	58.2	34	21	AAZ89642	Plasmid pUC19 prim
30	12.8	58.2	34	21	AAZ89642	Plasmid pUC19 prim
31	12.8	58.2	41	22	AA166435	Human thrombotic p
32	12.8	58.2	41	22	AA166435	Human thrombotic p
33	12.8	58.2	43	21	AAZ89643	Plasmid pUC19 prim
34	12.8	58.2	43	21	AAZ89643	Plasmid pUC19 prim
35	12.8	58.2	43	21	AAZ89644	Plasmid pUC19 prim
36	12.8	58.2	43	21	AAZ89644	Plasmid pUC19 prim
37	12.6	57.3	24	24	AB190430	Capture oligonucle
38	12.6	57.3	24	24	AB190430	Capture oligonucle
39	12.6	57.3	24	24	AB190431	Capture oligonucle
40	12.6	57.3	24	24	AB190431	Capture oligonucle
41	12.6	57.3	25	22	AAAD10725	Myobacterium tube
42	12.6	57.3	25	22	AAAD10725	Myobacterium tube
43	12.4	56.4	20	20	AAZ05939	PCR primer used to
44	12.4	56.4	20	20	AAZ05939	PCR primer used to
45	12.4	56.4	21	19	AAV73540	H. pylori vaca pro
46	12.4	56.4	21	19	AAV73540	H. pylori vaca pro
47	12.4	56.4	32	16	AAO80466	Primer (VUP2) com
48	12.4	56.4	32	16	AAO80466	Primer (VUP2) com
49	12.2	55.5	21	22	AAV96413	Human gene single
50	12.2	55.5	21	22	AAV96413	Human gene single
51	12.2	55.5	24	22	AAAD02190	BNVV replicase ge
52	12.2	55.5	24	22	AAAD02190	BNVV replicase ge
53	12.2	55.5	26	15	AAO5838	HCV detection prim
54	12.2	55.5	26	15	AAO5838	HCV detection prim
55	12.2	55.5	26	15	AAO5838	HCV detection prim
56	12.2	55.5	26	17	AAAT13284	Primer 1 for genom
57	12.2	55.5	26	17	AAAT13284	Primer 1 for genom
58	12.2	55.5	31	20	AAV83985	PCR primer C266 us
59	12.2	55.5	31	20	AAV83985	PCR primer C266 us
60	12.2	55.5	31	21	AAAI4934	PCR primer used to
61	12.2	55.5	31	21	AAAI4934	PCR primer used to
62	12.2	55.5	32	21	ABA98899	DNA sequence 7 rel
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64	12.2	55.5	33	18	AAV96347	Light chain 5' sen
65	12.2	55.5	33	18	AAV96347	Light chain 5' sen
66	12.2	55.5	37	22	AAV80208	PCR primer used to
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68	12.2	55.5	37	22	AAV55480	PCR primer used to
69	12.2	55.5	37	22	AAV55480	PCR primer used to
70	12.2	55.5	47	21	AAZ68554	Human map-related
71	12.2	55.5	47	21	AAZ68554	Human map-related
72	12	54.5	28	16	AAV08343	The human papillom
73	12	54.5	28	16	AAV08343	The human papillom
74	12	54.5	28	16	AAV08344	Antisense oligonuc
75	12	54.5	28	16	AAV08344	Antisense oligonuc
76	12	54.5	37	14	AAO48276	Vibrio proteolytic
77	12	54.5	37	14	AAO48276	Vibrio proteolytic
78	12	54.5	40	20	AAV02311	PCR primer #43. S
79	12	54.5	40	20	AAV02311	PCR primer #43. S
80	12	54.5	46	20	AAZ06995	Murine GABA B rece
81	12	54.5	46	20	AAZ06995	Murine GABA B rece
82	12	54.5	47	21	AAZ69147	Human map-related
			47	21	AAZ69147	Human map-related

83	11.8	53.6	24	24	ABL50125	Mouse telomerase c	156	11.4	51.8	40	14	AAQ33059	PCR primer #6 used
84	11.8	53.6	24	24	ABL50125	Mouse telomerase c	157	11.4	51.8	40	14	AAQ33438	Oligomer used in p
85	11.8	53.6	26	24	ABK49131	A. thaliana Activa	158	11.4	51.8	40	14	AAQ33438	Oligomer used in p
86	11.8	53.6	26	24	ABK49131	A. thaliana Activa	159	11.4	51.8	40	16	AAT01323	Prepro-allowycin
87	11.8	53.6	29	24	ABK49135	A. thaliana Activa	160	11.4	51.8	40	16	AAT01323	Prepro-allowycin
88	11.8	53.6	29	24	ABK49135	A. thaliana Activa	161	11.4	51.8	41	24	ABK23971	Synthetic PCR prim
89	11.8	53.6	40	21	AAZ95959	Polynucleotide seq	162	11.4	51.8	41	24	ABK23972	Synthetic PCR prim
90	11.8	53.6	40	21	AAZ95959	Polynucleotide seq	163	11.4	51.8	41	24	ABK23972	Synthetic PCR prim
91	11.8	53.6	45	16	AAO88181	Endorionuclease r	164	11.4	51.8	41	24	ABK23972	Synthetic PCR prim
92	11.8	53.6	45	16	AAO88181	Endorionuclease r	165	11.4	51.8	45	24	ABA95177	Linker used in the
93	11.6	52.7	19	21	AAZ75857	Human diallelic ma	166	11.4	51.8	45	24	ABA95177	Linker used in the
94	11.6	52.7	19	21	AAZ75857	Human diallelic ma	167	11.4	51.8	47	24	AAZ22537	Random RNA sequenc
95	11.6	52.7	20	20	AAZ06043	PCR primer used to	168	11.4	51.8	47	24	AAZ22537	Random RNA sequenc
96	11.6	52.7	20	20	AAZ06043	PCR primer used to	169	11.4	51.8	48	13	AAQ22423	Human V kappa spec
97	11.6	52.7	21	19	AAV57628	Exon 13 of an ENAC	170	11.4	51.8	48	13	AAQ22423	Human V kappa spec
98	11.6	52.7	21	19	AAV57628	Exon 13 of an ENAC	171	11.4	51.8	48	14	AAO44193	Probe Oligo-65 spe
99	11.6	52.7	21	20	AAK32063	MLH1 gene specific	172	11.4	51.8	48	14	AAO44193	Probe Oligo-65 spe
100	11.6	52.7	21	20	AAK32063	MLH1 gene specific	173	11.4	51.8	48	14	AAO44193	Probe Oligo-65 spe
101	11.6	52.7	30	24	ABK48802	SauAI adaptor Xs2	174	11.4	51.8	48	14	AAO50327	Human kappa light
102	11.6	52.7	30	24	ABK48802	SauAI adaptor Xs2	175	11.4	51.8	48	14	AAO50327	Human kappa light
103	11.6	52.7	38	22	AAH48754	Plasmid p35S-vacis	176	11.4	51.8	48	17	AAT37184	Human variable kap
104	11.6	52.7	38	22	AAH48754	Plasmid p35S-vacis	177	11.4	51.8	48	17	AAT37184	Human variable kap
105	11.6	52.7	38	23	ABK04044	Human NOGO Hammer	178	11.4	51.8	48	17	AAT37281	Human antibody kap
106	11.6	52.7	38	23	ABK04044	Human NOGO Hammer	179	11.4	51.8	48	18	AAV12576	Human antibody kap
107	11.6	52.7	41	19	AAV39482	Hairpin oligonucle	180	11.4	51.8	48	18	AAV12576	Probe Oligo-65 for
108	11.6	52.7	41	19	AAV39482	Hairpin oligonucle	181	11.4	51.8	48	18	AAT70526	Probe Oligo-65 for
109	11.6	52.7	47	21	AAZ69024	Human map-related	182	11.4	51.8	48	18	AAT70526	Human immunoglobul
110	11.6	52.7	47	21	AAZ69024	Human map-related	183	11.4	51.8	48	18	AAT73479	Human kappa light
111	11.4	51.8	18	16	AAO86666	NF-AT transcrip	184	11.4	51.8	48	18	AAT73479	Human kappa light
112	11.4	51.8	18	16	AAO86666	NF-AT transcrip	185	11.4	51.8	48	18	AAV38172	Probe Oligo-65 for
113	11.4	51.8	18	22	AAE31709	NF-AT-related prim	186	11.4	51.8	48	19	AAV38172	Probe Oligo-65 for
114	11.4	51.8	18	22	AAE31709	NF-AT-related prim	187	11.4	51.8	48	20	AAZ21964	Probe specific for
115	11.4	51.8	18	22	AAE31713	Human NF-ATc degen	188	11.4	51.8	48	20	AAZ21964	Probe specific for
116	11.4	51.8	18	22	AAE31713	Human NF-ATc degen	189	11.4	51.8	48	20	AAZ21964	Human kappa light
117	11.4	51.8	18	24	AAO34035	Reverse PCR primer	190	11.4	51.8	48	20	AAZ21964	Human kappa light
118	11.4	51.8	18	24	AAO34035	Reverse PCR primer	191	11.2	50.9	20	24	AAZ21964	Mutine SACT gene-s
119	11.4	51.8	20	24	ABN83710	Arthrobacter sp. d	192	11.2	50.9	20	24	AAZ21964	Mutine SACT gene-s
120	11.4	51.8	20	24	ABN83710	Arthrobacter sp. d	193	11.2	50.9	22	20	AAZ21964	GI tract binding p
121	11.4	51.8	25	21	AAO55320	Mouse activation-i	194	11.2	50.9	22	20	AAZ21964	Probe specific for
122	11.4	51.8	25	21	AAO55320	Mouse activation-i	195	11.2	50.9	24	17	AAT30622	Probe specific for
123	11.4	51.8	26	20	AAH84133	PCR primer for Ara	196	11.2	50.9	24	17	AAT30622	Human kappa light
124	11.4	51.8	26	20	AAH84133	PCR primer for Ara	197	11.2	50.9	25	21	AAZ55301	Human kappa light
125	11.4	51.8	27	24	ABL41271	Diabody antibody r	198	11.2	50.9	25	21	AAZ55301	Neisseria species
126	11.4	51.8	27	24	ABL41271	Diabody antibody r	199	11.2	50.9	26	22	AAE17297	Neisseria species
127	11.4	51.8	29	20	AAO55577	Mab 96-110 variabl	200	11.2	50.9	26	22	AAE17297	Information carryi
128	11.4	51.8	29	20	AAO55577	Mab 96-110 variabl	201	11.2	50.9	26	22	AAE17297	Information carryi
129	11.4	51.8	29	21	AAH11383	Tick-borne enceph	202	11.2	50.9	26	22	AAE17297	Information carryi
130	11.4	51.8	29	21	AAH11383	Tick-borne enceph	203	11.2	50.9	26	22	AAE17297	Information carryi
131	11.4	51.8	29	22	AAH10840	Human glucocerebro	204	11.2	50.9	29	22	AAE17297	Information carryi
132	11.4	51.8	29	22	AAH10840	Human glucocerebro	205	11.2	50.9	33	19	AAV49849	Information carryi
133	11.4	51.8	30	15	AAO74350	Human CD3 delta ch	206	11.2	50.9	33	19	AAV49849	Information carryi
134	11.4	51.8	30	15	AAO74350	Human CD3 delta ch	207	11.2	50.9	33	22	AAE28205	Information carryi
135	11.4	51.8	33	24	ABN81622	Fungal decaprenyl	208	11.2	50.9	33	22	AAE28205	Information carryi
136	11.4	51.8	33	24	ABN81622	Fungal decaprenyl	209	11.2	50.9	33	22	AAE28205	Information carryi
137	11.4	51.8	34	21	AAZ52278	PCR1 forward prime	210	11.2	50.9	18	24	ABN86174	A. salmonicida str
138	11.4	51.8	34	21	AAZ52278	PCR1 forward prime	211	11.2	50.9	18	24	ABN86174	A. salmonicida str
139	11.4	51.8	38	22	AAO87445	Sendai virus NheI	212	11.2	50.9	20	15	AAO55811	HCV detection prim
140	11.4	51.8	38	22	AAO87445	Sendai virus NheI	213	11.2	50.9	20	15	AAO55811	HCV detection prim
141	11.4	51.8	38	22	AAO87446	Sendai virus NheI	214	11.2	50.9	20	16	AAO80803	HCV genotype deter
142	11.4	51.8	38	22	AAO87446	Sendai virus NheI	215	11.2	50.9	20	16	AAO80803	HCV genotype deter
143	11.4	51.8	38	22	AAO87497	Sendai virus NheI	216	11.2	50.9	20	19	AAV69670	PTPRY gene specifi
144	11.4	51.8	38	22	AAO87497	Sendai virus NheI	217	11.2	50.9	20	19	AAV69670	PTPRY gene specifi
145	11.4	51.8	38	22	AAO87498	Sendai virus NheI	218	11.2	50.9	20	19	AAV37823	Human hepatitis vi
146	11.4	51.8	38	22	AAO87498	Sendai virus NheI	219	11.2	50.9	20	19	AAV37823	Human hepatitis vi
147	11.4	51.8	38	22	AAO33982	Sense primer #2 us	220	11.2	50.9	23	22	AAH76084	Rat CAR DNA amplif
148	11.4	51.8	38	24	AAO33982	Sense primer #2 us	221	11.2	50.9	23	22	AAH76084	Rat CAR DNA amplif
149	11.4	51.8	38	24	AAO33983	Antisense primer #	222	11.2	50.9	25	21	AAH39008	Brevibacterium fla
150	11.4	51.8	38	24	AAO33983	Antisense primer #	223	11.2	50.9	25	21	AAH39008	Brevibacterium fla
151	11.4	51.8	39	20	AAK37578	Human papilloma vi	224	11.2	50.9	25	21	AAK37578	PCR primer 5 speci
152	11.4	51.8	39	20	AAK37578	Human papilloma vi	225	11.2	50.9	25	24	ABO12058	Oligonucleotide ad
153	11.4	51.8	39	21	AAZ48186	HPV 16 LI expressi	226	11.2	50.9	25	24	ABO12058	Oligonucleotide ad
154	11.4	51.8	39	21	AAZ48186	HPV 16 LI expressi	227	11.2	50.9	26	22	AAH01449	blAEP-1 resistanc
155	11.4	51.8	40	14	AAQ33059	PCR primer #6 used	228	11.2	50.9	26	22	AAH01449	blAEP-1 resistanc

229	11	50.0	30	21	AA295613	Oligonucleotide M-	C 302	10.8	49.1	41	22	AA295613	Human ARE ITA int
C 230	11	50.0	30	21	AA295613	Oligonucleotide M-	C 303	10.8	49.1	41	22	AA295613	Human ARE ITA int
C 231	11	50.0	30	22	AA295640	Human CON202 G pro	C 304	10.8	49.1	41	24	AA295640	Human chemokine LP
C 232	11	50.0	30	22	AA295640	Human CON202 G pro	C 305	10.8	49.1	45	13	AA295640	Human chemokine LP
C 233	11	50.0	32	10	AA292279	Probe for 21 bp mo	C 306	10.8	49.1	45	13	AA292279	3' end of PCR-amp1
C 234	11	50.0	32	10	AA292279	Probe for 21 bp mo	C 307	10.8	49.1	47	15	AA292279	FelV gag/prot gene
C 235	11	50.0	32	18	AA295766	c-Ki-ras antisense	C 308	10.8	49.1	47	15	AA295766	FelV gag/prot gene
C 236	11	50.0	32	18	AA295766	c-Ki-ras antisense	C 309	10.8	49.1	47	20	AA295766	Human genome biall1
C 237	11	50.0	32	21	AA15021	PCR primer used to	C 310	10.8	49.1	47	20	AA15021	Human genome biall1
C 238	11	50.0	32	21	AA15021	PCR primer used to	C 311	10.8	49.1	47	21	AA15021	Human map-related
C 239	11	50.0	33	10	AA292277	Probe for 21 bp mo	C 312	10.8	49.1	47	21	AA292277	Human map-related
C 240	11	50.0	33	10	AA292277	Probe for 21 bp mo	C 313	10.8	49.1	47	21	AA292277	Human map-related
C 241	11	50.0	34	24	ABK88062	Biomebrane permea	C 314	10.8	49.1	47	21	ABK88062	Human map-related
C 242	11	50.0	34	24	ABK88062	Biomebrane permea	C 315	10.8	49.1	48	21	ABK88062	Hpv 83 ori DNA fra
C 243	11	50.0	36	14	AAQ48273	Vibrio campbellii	C 316	10.8	49.1	48	21	AAQ48273	Hpv 83 ori DNA fra
C 244	11	50.0	36	14	AAQ48273	Vibrio campbellii	C 317	10.8	49.1	49	21	AAQ48273	PCR primer-12 for
C 245	11	50.0	36	24	AA29711	Human BRCA1 gene a	C 318	10.8	49.1	49	21	AA29711	PCR primer-12 for
C 246	11	50.0	36	24	AA29711	Human BRCA1 gene a	C 319	10.8	49.1	50	21	AA29711	1467-00 PCR primer
C 247	11	50.0	37	20	AA291965	Porphyromonas ging	C 320	10.8	49.1	50	22	AA291965	1467-04 oligonucle
C 248	11	50.0	37	20	AA291965	Porphyromonas ging	C 321	10.8	49.1	50	22	AA291965	1467-04 oligonucle
C 249	11	50.0	37	22	AA291965	Linker oligonucleo	C 322	10.8	49.1	50	22	AA291965	Treponema pallidum
C 250	11	50.0	37	22	AA291965	Linker oligonucleo	C 323	10.8	49.1	50	24	AA291965	Treponema pallidum
C 251	11	50.0	37	24	ABK47047	Adenovirus adapter	C 324	10.8	49.1	50	24	ABK47047	Mycobacterium tube
C 252	11	50.0	37	24	ABK47047	Adenovirus adapter	C 325	10.8	49.1	50	24	ABK47047	Mycobacterium tube
C 253	11	50.0	40	18	AA297295	Path-starting PCR	C 326	10.8	49.1	17	21	AA297295	PCR primer CHP1338
C 254	11	50.0	40	18	AA297295	Path-starting PCR	C 327	10.6	48.2	17	21	AA297295	HCV isolating modu
C 255	11	50.0	43	20	AA209340	Pseudomonas sp. st	C 328	10.6	48.2	17	21	AA209340	HCV isolating modu
C 256	11	50.0	43	20	AA209340	Pseudomonas sp. st	C 329	10.6	48.2	18	19	AA209340	HCV isolating modu
C 257	11	50.0	43	21	AA297466	Mycobacterium tube	C 330	10.6	48.2	18	19	AA297466	Hepatitis C virus
C 258	11	50.0	43	21	AA297466	Mycobacterium tube	C 331	10.6	48.2	18	21	AA297466	Hepatitis C virus
C 259	11	50.0	43	21	AA297466	Reverse primer 204	C 332	10.6	48.2	18	21	AA297466	Hepatitis C virus
C 260	11	50.0	43	21	AA297466	Reverse primer 204	C 333	10.6	48.2	20	13	AA297466	Microsatellite rep
C 261	11	50.0	46	16	AAQ83070	HIV hammerhead mot	C 334	10.6	48.2	20	13	AAQ83070	Microsatellite rep
C 262	11	50.0	46	16	AAQ83070	HIV hammerhead mot	C 335	10.6	48.2	20	15	AAQ83070	primer pair 8A CST
C 263	11	50.0	46	16	AAQ83070	HIV hammerhead mot	C 336	10.6	48.2	20	15	AAQ83070	primer pair 8A CST
C 264	11	50.0	46	16	AAQ83070	HIV hammerhead mot	C 337	10.6	48.2	20	15	AAQ83070	Antisense oligonuc
C 265	11	50.0	47	21	AA267760	Human map-related	C 338	10.6	48.2	20	15	AA267760	Antisense oligonuc
C 266	11	50.0	47	21	AA267760	Human map-related	C 339	10.6	48.2	20	17	AA267760	Hepatitis C virus
C 267	11	50.0	48	17	AA267760	Human map-related	C 340	10.6	48.2	20	17	AA267760	Hepatitis C virus
C 268	11	50.0	48	17	AA267760	Secretory phosphol	C 341	10.6	48.2	20	21	AA267760	Nucleotide sequenc
C 269	11	50.0	48	22	AA267760	Secretory phosphol	C 342	10.6	48.2	20	21	AA267760	Nucleotide sequenc
C 270	11	50.0	48	22	AA267760	Multiplex PCR prim	C 343	10.6	48.2	20	21	AA267760	Forward primer for
C 271	11	50.0	48	22	AA267760	Multiplex PCR prim	C 344	10.6	48.2	20	21	AA267760	Forward primer for
C 272	11	50.0	48	22	AA267760	Dystrophin exon 47	C 345	10.6	48.2	20	24	AA267760	Human chromosome 1
C 273	11	50.0	50	20	AA222993	5' primer used for	C 346	10.6	48.2	20	24	AA222993	Human chromosome 1
C 274	11	50.0	50	20	AA222993	5' primer used for	C 347	10.6	48.2	21	17	AA222993	Laccase gene forwa
C 275	10.8	49.1	20	16	AAQ91343	Chromosome 11 (loc	C 348	10.6	48.2	21	17	AAQ91343	Laccase gene forwa
C 276	10.8	49.1	20	16	AAQ91343	Chromosome 11 (loc	C 349	10.6	48.2	21	19	AAQ91343	Hepatitis C virus
C 277	10.8	49.1	20	21	AA267760	Dog genomic marker	C 350	10.6	48.2	21	19	AA267760	Hepatitis C virus
C 278	10.8	49.1	20	21	AA267760	Dog genomic marker	C 351	10.6	48.2	21	21	AA267760	Primer used to ver
C 279	10.8	49.1	22	15	AAQ63679	PCR primer for vB3	C 352	10.6	48.2	21	21	AAQ63679	A. gossypii antifu
C 280	10.8	49.1	22	15	AAQ63679	PCR primer for vB3	C 353	10.6	48.2	21	22	AAQ63679	A. gossypii antifu
C 281	10.8	49.1	23	13	AAQ34356	Downstream PCR pri	C 354	10.6	48.2	21	22	AAQ34356	Geneticin resistan
C 282	10.8	49.1	23	13	AAQ34356	Downstream PCR pri	C 355	10.6	48.2	21	22	AAQ34356	Geneticin resistan
C 283	10.8	49.1	23	18	AA297030	Presentin-2 alter	C 356	10.6	48.2	21	22	AA297030	Bacterial gene PKS
C 284	10.8	49.1	23	18	AA297030	Presentin-2 alter	C 357	10.6	48.2	21	23	AA297030	Bacterial gene PKS
C 285	10.8	49.1	25	21	AA268608	Bacteriophage 3A O	C 358	10.6	48.2	21	23	AA268608	Olfactory receptor
C 286	10.8	49.1	25	21	AA268608	Bacteriophage 3A O	C 359	10.6	48.2	21	24	AA268608	Olfactory receptor
C 287	10.8	49.1	26	24	ABK86992	RCR selection prim	C 360	10.6	48.2	21	24	ABK86992	AsbVya gossypii ge
C 288	10.8	49.1	26	24	ABK86992	RCR selection prim	C 361	10.6	48.2	21	24	ABK86992	AsbVya gossypii ge
C 289	10.8	49.1	28	20	AA208851	Human NIS PCR prim	C 362	10.6	48.2	21	24	AA208851	Immunostimulatory
C 290	10.8	49.1	28	20	AA208851	Human NIS PCR prim	C 363	10.6	48.2	22	21	AA208851	Immunostimulatory
C 291	10.8	49.1	28	23	AB150501	Cosmid clones enco	C 364	10.6	48.2	22	21	AB150501	Hepatitis C virus
C 292	10.8	49.1	28	23	AB150501	Cosmid clones enco	C 365	10.6	48.2	22	22	AB150501	Hepatitis C virus
C 293	10.8	49.1	32	14	AAQ44873	3' PCR primer OT-1	C 366	10.6	48.2	22	22	AAQ44873	GAPDH PCR primer #
C 294	10.8	49.1	32	14	AAQ44873	3' PCR primer OT-1	C 367	10.6	48.2	22	24	AAQ44873	GAPDH PCR primer #
C 295	10.8	49.1	34	19	AAV12058	HIV-2 vcp env gene	C 368	10.6	48.2	22	24	AAV12058	Myobacterium tube
C 296	10.8	49.1	34	19	AAV12058	HIV-2 vcp env gene	C 369	10.6	48.2	23	21	AAV12058	Myobacterium tube
C 297	10.8	49.1	35	21	AA293756	Putative rho indep	C 370	10.6	48.2	23	21	AA293756	PCR primer specifi
C 298	10.8	49.1	35	21	AA293756	Putative rho indep	C 371	10.6	48.2	23	22	AA293756	PCR primer specifi
C 299	10.8	49.1	38	24	AA28610	Human HSV-1 UL48 g	C 372	10.6	48.2	23	22	AA28610	OA/TA transporter
C 300	10.8	49.1	38	24	AA28610	Human HSV-1 UL48 g	C 373	10.6	48.2	23	22	AA28610	OA/TA transporter
C 301	10.8	49.1	41	22	AA28655	Human ARE ITA int	C 374	10.6	48.2	23	22	AA28655	OA/TA transporter

375	10.6	48.2	24	15	AA064954	Antisense oligonuc	C	448	10.6	48.2	36	21	AAC61518	PCR primer used to
376	10.6	48.2	24	15	AA064954	Antisense oligonuc	C	449	10.6	48.2	36	21	AAC62477	Barley D-thordein p
377	10.6	48.2	24	15	AAV39105	Primer CYP2D6R us	C	450	10.6	48.2	36	21	AA062477	Barley D-thordein p
378	10.6	48.2	24	19	AAV39105	Primer CYP2D6R us	C	451	10.6	48.2	36	21	AAA29447	Hepatitis C virus
379	10.6	48.2	24	20	AAZ18598	Primer for ASTH1 p	C	452	10.6	48.2	37	20	AAA29447	Hepatitis C virus
380	10.6	48.2	24	20	AAZ18598	Primer for ASTH1 p	C	453	10.6	48.2	37	20	AAZ09343	Pseudomonas sp. st
381	10.6	48.2	24	21	AAAB7584	Rat hepatocyte car	C	454	10.6	48.2	37	20	AAZ09343	Pseudomonas sp. st
382	10.6	48.2	24	21	AAAB7584	Rat hepatocyte car	C	455	10.6	48.2	37	20	AAZ09343	Pseudomonas sp. st
383	10.6	48.2	24	21	AAAB80505	ASTH1 polymorphic	C	456	10.6	48.2	37	20	AAZ09343	Pseudomonas sp. st
384	10.6	48.2	24	21	AAAB80505	ASTH1 polymorphic	C	457	10.6	48.2	37	22	AAAF27816	Human HFE gene wil
385	10.6	48.2	24	22	AAAD19054	Hepatitis C virus	C	458	10.6	48.2	37	22	AAAF27816	Human HFE gene wil
386	10.6	48.2	24	22	AAAD19054	Hepatitis C virus	C	459	10.6	48.2	37	22	AAAF27816	Human HFE gene wil
387	10.6	48.2	24	22	AAAH01399	aph(3')-Ia resista	C	460	10.6	48.2	37	22	AAAF27816	Human HFE gene wil
388	10.6	48.2	24	22	AAAH01399	aph(3')-Ia resista	C	461	10.6	48.2	38	16	AAO90472	Human Kunitz-type
389	10.6	48.2	24	24	ABO01236	Oligonucleotide ad	C	462	10.6	48.2	38	16	AAO90472	Human Kunitz-type
390	10.6	48.2	24	24	ABO01236	Oligonucleotide ad	C	463	10.6	48.2	38	23	ABK04312	Human NOGO Hammett
391	10.6	48.2	24	24	ABO06397	Oligonucleotide ad	C	464	10.6	48.2	38	23	ABK04312	Human NOGO Hammett
392	10.6	48.2	24	24	ABO06397	Oligonucleotide ad	C	465	10.6	48.2	38	24	ABK58497	Human CLIC1 gene e
393	10.6	48.2	24	24	ABO06438	Oligonucleotide ad	C	466	10.6	48.2	38	24	ABK58497	Human CLIC1 gene e
394	10.6	48.2	24	24	ABO06438	Oligonucleotide ad	C	467	10.6	48.2	38	24	ABK19594	Human ERG hammethe
395	10.6	48.2	24	24	ABO06438	Oligonucleotide ad	C	468	10.6	48.2	38	24	ABK19594	Human ERG hammethe
396	10.6	48.2	24	24	ABL46270	Hepatitis C virus	C	469	10.6	48.2	38	24	ABK19628	Human ERG hammethe
397	10.6	48.2	24	24	ABL46270	Hepatitis C virus	C	470	10.6	48.2	38	24	ABK19628	Human ERG hammethe
398	10.6	48.2	24	24	ABD23639	Human CYP2D6 exon	C	471	10.6	48.2	39	20	AAK03234	PCR primer used to
399	10.6	48.2	25	21	AAA96551	Forward PCR primer	C	472	10.6	48.2	39	20	AAK03234	PCR primer used to
400	10.6	48.2	25	21	AAA96551	Forward PCR primer	C	473	10.6	48.2	40	12	AAQ13881	HFV 18 subregion E
401	10.6	48.2	25	21	AAA96551	Forward PCR primer	C	474	10.6	48.2	40	12	AAQ13881	HFV 18 subregion E
402	10.6	48.2	25	21	AAA96551	Forward PCR primer	C	475	10.6	48.2	41	21	AAO88115	Flavivirus nonstru
403	10.6	48.2	25	21	AAA74620	HCV-specific ampli	C	476	10.6	48.2	41	21	AAO88115	Flavivirus nonstru
404	10.6	48.2	25	21	AAA74620	HCV-specific ampli	C	477	10.6	48.2	41	21	AAO88115	Flavivirus nonstru
405	10.6	48.2	25	21	AAA52569	Oligonucleotide SE	C	478	10.6	48.2	41	24	AAAS18045	Human polypeptide-
406	10.6	48.2	25	21	AAA52569	Oligonucleotide SE	C	479	10.6	48.2	41	24	AAAS18045	Human polypeptide-
407	10.6	48.2	25	21	AAA52570	Oligonucleotide SE	C	480	10.6	48.2	41	24	AAAS18050	Human polypeptide-
408	10.6	48.2	25	21	AAA52570	Oligonucleotide SE	C	481	10.6	48.2	42	21	AAAS18050	Human polypeptide-
409	10.6	48.2	26	21	AAA74622	HCV-specific ampli	C	482	10.6	48.2	42	21	AAAS97871	BBV L1 protein pri
410	10.6	48.2	26	21	AAA74622	HCV-specific ampli	C	483	10.6	48.2	43	20	AAV84775	Antibody kappa cha
411	10.6	48.2	27	15	AA064949	Antisense oligonuc	C	484	10.6	48.2	43	20	AAV84775	Antibody kappa cha
412	10.6	48.2	27	15	AA064949	Antisense oligonuc	C	485	10.6	48.2	43	21	AAV75927	PCR primer used to
413	10.6	48.2	27	15	AA064955	Antisense oligonuc	C	486	10.6	48.2	43	21	AAV75927	PCR primer used to
414	10.6	48.2	27	15	AA064955	Antisense oligonuc	C	487	10.6	48.2	43	21	AAV75927	PCR primer used to
415	10.6	48.2	27	15	AA064955	Antisense oligonuc	C	488	10.6	48.2	43	21	AAV75927	PCR primer used to
416	10.6	48.2	27	21	AAAO7987	Subcellular locali	C	489	10.6	48.2	43	21	AAV75927	PCR primer used to
417	10.6	48.2	27	21	AAAO7987	Subcellular locali	C	490	10.6	48.2	43	21	AAV75927	PCR primer used to
418	10.6	48.2	27	22	AAAF61159	Single chain Fv an	C	491	10.6	48.2	44	19	AAV62488	Reverse primer 204
419	10.6	48.2	29	21	AAZ61110	PCR primer used to	C	492	10.6	48.2	44	19	AAV62488	Reverse primer 204
420	10.6	48.2	29	21	AAZ61110	PCR primer used to	C	493	10.6	48.2	45	19	AAV27897	Op 162 gene PA sig
421	10.6	48.2	29	21	AAZ61110	PCR primer used to	C	494	10.6	48.2	45	19	AAV27897	Op 162 gene PA sig
422	10.6	48.2	29	22	AAI68457	Plasmid pSV-Hir-C	C	495	10.6	48.2	45	24	AAV27897	Rat GALK2 receptor
423	10.6	48.2	30	13	AAO20877	Immunostimulatory	C	496	10.6	48.2	45	24	AAV27897	Rat GALK2 receptor
424	10.6	48.2	30	13	AAO20877	Immunostimulatory	C	497	10.6	48.2	48	20	AAZ30769	Rat galanin recept
425	10.6	48.2	30	15	AA064950	Antisense oligonuc	C	498	10.6	48.2	48	20	AAZ30769	Rat galanin recept
426	10.6	48.2	30	15	AA064950	Antisense oligonuc	C	499	10.6	48.2	48	20	AAZ30769	Rat galanin recept
427	10.6	48.2	30	17	AAAT38779	MPMV primer 1 for	C	500	10.6	48.2	48	20	AAZ30769	Rat galanin recept
428	10.6	48.2	30	17	AAAT38779	MPMV primer 1 for	C	501	10.6	48.2	48	24	AAAS17386	Human CD4 N-termi
429	10.6	48.2	30	21	AAZ93958	M. tuberculosis ca	C	502	10.6	48.2	48	24	AAAS17386	Human CD4 N-termi
430	10.6	48.2	30	21	AAZ93958	M. tuberculosis ca	C	503	10.6	48.2	48	24	AAAS17391	Human CD4 N-termi
431	10.6	48.2	30	24	ABK85995	Dendritic cell sti	C	504	10.6	48.2	48	24	AAAS17391	Human CD4 N-termi
432	10.6	48.2	30	24	ABK85995	Dendritic cell sti	C	505	10.6	48.2	50	18	AAAT69973	FLPV spike (S) gen
433	10.6	48.2	30	24	ABK85995	Dendritic cell sti	C	506	10.6	48.2	50	18	AAAT69973	FLPV spike (S) gen
434	10.6	48.2	30	24	ABK85995	Dendritic cell sti	C	507	10.6	48.2	50	21	AAAB89757	HCV RNA promoter p
435	10.6	48.2	31	21	AAA99306	Oligonucleotide E	C	508	10.6	48.2	50	21	AAAB89757	HCV RNA promoter p
436	10.6	48.2	31	21	AAA99306	Oligonucleotide E	C	509	10.6	48.2	50	21	AAAB89757	HCV RNA promoter p
437	10.6	48.2	32	20	AAK61004	PCR primer for HPV	C	510	10.6	48.2	50	21	AAAB89757	HCV RNA promoter p
438	10.6	48.2	32	20	AAK61004	PCR primer for HPV	C	511	10.6	48.2	50	21	AAAB89757	HCV RNA promoter p
439	10.6	48.2	33	13	AAO30077	Sequence of instal	C	512	10.6	48.2	50	21	AAAB89757	HCV RNA promoter p
440	10.6	48.2	33	13	AAO30077	Sequence of instal	C	513	10.6	48.2	50	21	AAAB89757	HCV RNA promoter p
441	10.6	48.2	34	21	AAAC60374	Primer CAMH-UP. S	C	514	10.6	48.2	50	22	AAH23740	Oligonucleotide #4
442	10.6	48.2	34	21	AAAC60374	Primer CAMH-UP. S	C	515	10.6	48.2	50	22	AAH23740	Oligonucleotide #4
443	10.6	48.2	34	21	AAAB30489	C. tropicalis CYP5	C	516	10.6	48.2	50	22	AAH23740	Oligonucleotide #4
444	10.6	48.2	34	21	AAAB30489	C. tropicalis CYP5	C	517	10.6	48.2	50	22	AAH23740	Oligonucleotide #4
445	10.6	48.2	34	21	ABK31808	Candida tropicalis	C	518	10.6	48.2	50	22	AAH23740	Oligonucleotide #4
446	10.6	48.2	34	21	ABK31808	Candida tropicalis	C	519	10.6	48.2	50	22	AAH23740	Oligonucleotide #4
447	10.6	48.2	36	21	AAAC61518	PCR primer used to	C	520	10.6	48.2	50	22	AAH23740	Oligonucleotide #4

521	10.4	47.3	13	23	ABH56602	Oligonucleotide SE	C 594	10.4	47.3	24	24	ABQ03783	Oligonucleotide ad
C 522	10.4	47.3	13	23	ABH56602	Oligonucleotide SE	595	10.4	47.3	24	24	AB184166	Capture oligonucle
C 523	10.4	47.3	13	23	ABH56603	Oligonucleotide SE	C 596	10.4	47.3	24	24	AB184166	Capture oligonucle
C 524	10.4	47.3	13	23	ABH56603	Oligonucleotide SE	C 597	10.4	47.3	24	24	AB184167	Capture oligonucle
C 525	10.4	47.3	14	20	AA21642	Integrin alpha 6 s	C 598	10.4	47.3	24	24	AB184167	Capture oligonucle
C 526	10.4	47.3	14	20	AA21642	Integrin alpha 6 s	C 599	10.4	47.3	24	24	AB184167	Capture oligonucle
C 527	10.4	47.3	16	21	AA61730	Primer for a gene	C 600	10.4	47.3	24	24	AB184472	Capture oligonucle
C 528	10.4	47.3	16	21	AA61730	Primer for a gene	C 601	10.4	47.3	24	24	AB184472	Capture oligonucle
C 529	10.4	47.3	16	22	AA506518	Mouse microglia an	C 602	10.4	47.3	24	24	AB184473	Capture oligonucle
C 530	10.4	47.3	16	22	AA506518	Mouse microglia an	C 603	10.4	47.3	24	24	AB184473	Capture oligonucle
C 531	10.4	47.3	17	20	AA20792	Integrin alpha 6 s	C 604	10.4	47.3	24	24	AB184473	Capture oligonucle
C 532	10.4	47.3	17	20	AA20792	Integrin alpha 6 s	C 605	10.4	47.3	25	24	AB184473	Capture oligonucle
C 533	10.4	47.3	17	20	AA20793	Integrin alpha 6 s	C 606	10.4	47.3	25	24	AB184473	Capture oligonucle
C 534	10.4	47.3	17	20	AA20793	Integrin alpha 6 s	C 607	10.4	47.3	26	16	AA709068	Immunostimulatory
C 535	10.4	47.3	18	22	AA796681	Human Akt-3 antis	C 608	10.4	47.3	26	16	AA709068	Immunostimulatory
C 536	10.4	47.3	18	22	AA796681	Human Akt-3 antis	C 609	10.4	47.3	26	16	AA709068	Immunostimulatory
C 537	10.4	47.3	20	16	AA085909	Primer SS20 for M1	C 610	10.4	47.3	26	24	AB184473	Immunostimulatory
C 538	10.4	47.3	20	16	AA085909	Primer SS20 for M1	C 611	10.4	47.3	27	22	AAH37939	Immunostimulatory
C 539	10.4	47.3	20	18	AAV06723	M13mp2 Phage DNA P	C 612	10.4	47.3	27	22	AAH37939	Immunostimulatory
C 540	10.4	47.3	20	18	AAV06723	M13mp2 Phage DNA P	C 613	10.4	47.3	28	22	AAH37939	Immunostimulatory
C 541	10.4	47.3	20	19	AAV19469	Primer used to amp	C 614	10.4	47.3	28	22	AAH37939	Immunostimulatory
C 542	10.4	47.3	20	19	AAV19469	Primer used to amp	C 615	10.4	47.3	29	20	AAH37939	Immunostimulatory
C 543	10.4	47.3	20	21	AA081302	Mouse apoptosis-re	C 616	10.4	47.3	29	20	AAH37939	Immunostimulatory
C 544	10.4	47.3	20	21	AA081302	Mouse apoptosis-re	C 617	10.4	47.3	29	20	AAH37939	Immunostimulatory
C 545	10.4	47.3	20	21	AA081302	Hepatitis B virus	C 618	10.4	47.3	29	20	AAH37939	Immunostimulatory
C 546	10.4	47.3	20	21	AA081302	Hepatitis B virus	C 619	10.4	47.3	29	20	AAH37939	Immunostimulatory
C 547	10.4	47.3	20	21	AA081302	Hepatitis B virus	C 620	10.4	47.3	29	20	AAH37939	Immunostimulatory
C 548	10.4	47.3	20	24	ABK92281	Human tumour suppr	C 621	10.4	47.3	29	21	AAH37939	Immunostimulatory
C 549	10.4	47.3	20	24	ABK92282	Human tumour suppr	C 622	10.4	47.3	29	21	AAH37939	Immunostimulatory
C 550	10.4	47.3	20	24	ABK92282	Human tumour suppr	C 623	10.4	47.3	29	21	AAH37939	Immunostimulatory
C 551	10.4	47.3	20	24	ABK92282	Human tumour suppr	C 624	10.4	47.3	29	24	AAH37939	Immunostimulatory
C 552	10.4	47.3	20	24	ABK92282	Human caspase 7 ph	C 625	10.4	47.3	30	21	AAH37939	Immunostimulatory
C 553	10.4	47.3	20	24	ABK92282	Human caspase 7 ph	C 626	10.4	47.3	30	21	AAH37939	Immunostimulatory
C 554	10.4	47.3	20	24	ABK92282	Human caspase 7 ph	C 627	10.4	47.3	31	15	AAH37939	Immunostimulatory
C 555	10.4	47.3	20	24	ABK92282	Human caspase 7 ph	C 628	10.4	47.3	31	15	AAH37939	Immunostimulatory
C 556	10.4	47.3	20	24	ABK92282	Capture oligonucle	C 629	10.4	47.3	31	15	AAH37939	Immunostimulatory
C 557	10.4	47.3	20	24	ABK92282	Capture oligonucle	C 630	10.4	47.3	31	15	AAH37939	Immunostimulatory
C 558	10.4	47.3	20	24	ABK92282	Capture oligonucle	C 631	10.4	47.3	31	15	AAH37939	Immunostimulatory
C 559	10.4	47.3	20	24	ABK92282	Capture oligonucle	C 632	10.4	47.3	31	15	AAH37939	Immunostimulatory
C 560	10.4	47.3	21	13	AAQ28662	ORH1 SENSE primer.	C 633	10.4	47.3	31	17	AAH37939	Immunostimulatory
C 561	10.4	47.3	21	13	AAQ28662	ORH1 SENSE primer.	C 634	10.4	47.3	31	17	AAH37939	Immunostimulatory
C 562	10.4	47.3	21	14	AAQ48548	HPV E6/7 region pr	C 635	10.4	47.3	31	17	AAH37939	Immunostimulatory
C 563	10.4	47.3	21	14	AAQ48548	HPV E6/7 region pr	C 636	10.4	47.3	31	18	AAH37939	Immunostimulatory
C 564	10.4	47.3	21	14	AAQ48548	HPV E6/7 region pr	C 637	10.4	47.3	31	18	AAH37939	Immunostimulatory
C 565	10.4	47.3	21	14	AAQ48548	HPV E6/7 region pr	C 638	10.4	47.3	31	19	AAH37939	Immunostimulatory
C 566	10.4	47.3	21	20	AAZ20523	PCR primer for adh	C 639	10.4	47.3	31	19	AAH37939	Immunostimulatory
C 567	10.4	47.3	21	20	AAZ20523	PCR primer for adh	C 640	10.4	47.3	31	19	AAH37939	Immunostimulatory
C 568	10.4	47.3	21	20	AAZ20523	Human DLST gene sp	C 641	10.4	47.3	31	19	AAH37939	Immunostimulatory
C 569	10.4	47.3	21	21	AAZ20523	Human DLST gene sp	C 642	10.4	47.3	31	19	AAH37939	Immunostimulatory
C 570	10.4	47.3	21	21	AAZ20523	Human uterine neck	C 643	10.4	47.3	31	19	AAH37939	Immunostimulatory
C 571	10.4	47.3	21	21	AAZ20523	Human uterine neck	C 644	10.4	47.3	31	20	AAH37939	Immunostimulatory
C 572	10.4	47.3	21	21	AAZ20523	Human uterine neck	C 645	10.4	47.3	31	20	AAH37939	Immunostimulatory
C 573	10.4	47.3	21	21	AAZ20523	Human uterine neck	C 646	10.4	47.3	31	20	AAH37939	Immunostimulatory
C 574	10.4	47.3	21	24	AAK99082	S. aureus 16S H-7,	C 647	10.4	47.3	31	20	AAH37939	Immunostimulatory
C 575	10.4	47.3	22	16	AAK99082	S. aureus 16S H-7,	C 648	10.4	47.3	31	20	AAH37939	Immunostimulatory
C 576	10.4	47.3	22	16	AAK99082	Primer lacZ 560 fo	C 649	10.4	47.3	31	20	AAH37939	Immunostimulatory
C 577	10.4	47.3	22	16	AAK99082	Primer lacZ 560 fo	C 650	10.4	47.3	31	20	AAH37939	Immunostimulatory
C 578	10.4	47.3	22	20	AAZ32481	ROSA beta-geo vect	C 651	10.4	47.3	31	21	AAH37939	Immunostimulatory
C 579	10.4	47.3	22	20	AAZ32481	ROSA beta-geo vect	C 652	10.4	47.3	31	21	AAH37939	Immunostimulatory
C 580	10.4	47.3	22	22	AAH44610	E. coli lacZ RT-PC	C 653	10.4	47.3	31	21	AAH37939	Immunostimulatory
C 581	10.4	47.3	22	22	AAH44610	lacZ gene PCR prim	C 654	10.4	47.3	31	21	AAH37939	Immunostimulatory
C 582	10.4	47.3	22	22	AAH44610	lacZ gene PCR prim	C 655	10.4	47.3	31	21	AAH37939	Immunostimulatory
C 583	10.4	47.3	23	20	AAH86639	Human chromosome 1	C 656	10.4	47.3	31	21	AAH37939	Immunostimulatory
C 584	10.4	47.3	23	20	AAH86639	Human chromosome 1	C 657	10.4	47.3	31	21	AAH37939	Immunostimulatory
C 585	10.4	47.3	23	22	AAH86639	Human DAPI CDNA 5	C 658	10.4	47.3	31	21	AAH37939	Immunostimulatory
C 586	10.4	47.3	23	22	AAH86639	Human DAPI CDNA 5	C 659	10.4	47.3	31	21	AAH37939	Immunostimulatory
C 587	10.4	47.3	24	15	AAH86639	Bacillus thuringie	C 660	10.4	47.3	31	22	AAH37939	Immunostimulatory
C 588	10.4	47.3	24	15	AAH86639	Bacillus thuringie	C 661	10.4	47.3	31	22	AAH37939	Immunostimulatory
C 589	10.4	47.3	24	17	AAH86639	cryII gene primer	C 662	10.4	47.3	31	22	AAH37939	Immunostimulatory
C 590	10.4	47.3	24	17	AAH86639	cryII gene primer	C 663	10.4	47.3	31	22	AAH37939	Immunostimulatory
C 591	10.4	47.3	24	22	AAH86639	Immunostimulatory	C 664	10.4	47.3	33	14	AAH37939	Immunostimulatory
C 592	10.4	47.3	24	22	AAH86639	Immunostimulatory	C 665	10.4	47.3	33	18	AAH37939	Immunostimulatory
C 593	10.4	47.3	24	24	ABQ03783	Oligonucleotide ad	C 666	10.4	47.3	33	18	AAH37939	Immunostimulatory

667	10.4	47.3	33	20	AA35405	Probe for DNA enco	C	740	10.4	47.3	48	21	AA292895	Sindbis virus geno
668	10.4	47.3	33	20	AA35405	Probe for DNA enco	C	741	10.4	47.3	48	22	AA660417	FGF receptor 3 lig
669	10.4	47.3	33	22	AAH41200	PCR primer ADU001.	C	742	10.4	47.3	48	22	AA660417	FGF receptor 3 lig
670	10.4	47.3	33	22	AAH41200	PCR primer ADU001.	C	743	10.4	47.3	48	22	AA672714	Human PRO polypept
671	10.4	47.3	37	14	AAQ48279	Vibrio parahemoly	C	744	10.4	47.3	48	22	AA672714	Human PRO polypept
672	10.4	47.3	37	14	AAQ48279	Vibrio parahemoly	C	745	10.4	47.3	48	22	AA672714	Alphavirus related
673	10.4	47.3	38	24	AA167999	A/teal/HK/312/97	C	746	10.4	47.3	48	24	AA138775	Alphavirus related
674	10.4	47.3	38	24	AA167999	A/teal/HK/312/97	C	747	10.4	47.3	48	24	ABK46241	Sindbis virus geno
675	10.4	47.3	39	17	AA140080	Primer for bcl-XS	C	748	10.4	47.3	48	24	ABK46241	Sindbis virus geno
676	10.4	47.3	39	17	AA140080	Primer for bcl-XS	C	749	10.4	47.3	48	24	AAH99927	Sindbis virus geno
677	10.4	47.3	39	21	AAH47123	Chlamydia pneumoni	C	750	10.4	47.3	48	24	AAH99927	Primer 2 used to a
678	10.4	47.3	39	21	AAH47123	Chlamydia pneumoni	C	751	10.4	47.3	48	24	ABH03387	Primer 2 used to a
679	10.4	47.3	39	21	AAH47123	Chlamydia pneumoni	C	752	10.4	47.3	48	24	ABH03387	Sindbis virus nons
680	10.4	47.3	40	14	AA050313	Detection probe 5.	C	753	10.4	47.3	49	21	AAA09560	Sindbis virus nons
681	10.4	47.3	40	15	AA053472	Detection probe 5.	C	754	10.4	47.3	49	21	AAA09560	Detection of nucle
682	10.4	47.3	40	15	AA053472	Probe THM13.3. Sy	C	755	10.4	47.3	50	18	AAV77788	Stephylococcus aur
683	10.4	47.3	40	15	AA054237	DNA sequence prepn	C	756	10.4	47.3	50	18	AAV77788	Stephylococcus aur
684	10.4	47.3	40	15	AA054237	DNA sequence prepn	C	757	10.4	47.3	50	21	AAH74409	Human bone marrow
685	10.4	47.3	40	18	AA147465	Foldback triplex f	C	758	10.4	47.3	50	21	AAH74409	Human bone marrow
686	10.4	47.3	40	18	AA147465	Foldback triplex f	C	759	10.4	47.3	50	22	AA130444	Human bone marrow
687	10.4	47.3	40	21	AA295865	Poly nucleotide seq	C	760	10.4	47.3	50	22	AA130444	Human SNP oligonc
688	10.4	47.3	40	21	AA295865	Poly nucleotide seq	C	761	10.4	47.3	50	22	AA130444	Human SNP oligonc
689	10.4	47.3	40	21	AA295865	Poly nucleotide seq	C	762	10.4	47.3	50	22	AA130444	Human SNP oligonc
690	10.4	47.3	40	24	ABN88576	Isoprenoid related	C	763	10.2	46.4	14	14	AA043637	Human SNP oligonc
691	10.4	47.3	40	24	ABN88576	Isoprenoid related	C	764	10.2	46.4	14	14	AA043637	5' PCR primer Cel-
692	10.4	47.3	40	24	ABN88576	Isoprenoid related	C	765	10.2	46.4	17	19	AAV95838	5' PCR primer Cel-
693	10.4	47.3	40	24	ABN88576	Isoprenoid related	C	766	10.2	46.4	17	19	AAV95838	Solanidine glucosy
694	10.4	47.3	40	24	ABN88576	Isoprenoid related	C	767	10.2	46.4	17	21	AAA36226	Human genomic SNP
695	10.4	47.3	41	13	AAQ31831	Green/red click be	C	768	10.2	46.4	17	21	AAA36226	Human genomic SNP
696	10.4	47.3	41	13	AAQ31831	Green/red click be	C	769	10.2	46.4	17	21	AAA36226	Human genomic SNP
697	10.4	47.3	41	13	AAQ31831	Probe binding regi	C	770	10.2	46.4	17	21	AAA36237	Human genomic SNP
698	10.4	47.3	41	13	AAQ31831	Probe binding regi	C	771	10.2	46.4	18	24	AB135558	Immunostimulatory
699	10.4	47.3	41	13	AAQ31831	Probe GGP105-145.	C	772	10.2	46.4	18	24	AB135558	Immunostimulatory
700	10.4	47.3	43	18	AA147467	Foldback triplex f	C	773	10.2	46.4	20	14	AA048563	HPV E6/7 region pr
701	10.4	47.3	43	18	AA147467	Foldback triplex f	C	774	10.2	46.4	20	14	AA048563	HPV E6/7 region pr
702	10.4	47.3	43	22	AAE89694	Probe used to iden	C	775	10.2	46.4	20	15	AA065418	Primer to amplify
703	10.4	47.3	43	22	AAE89694	Probe used to iden	C	776	10.2	46.4	20	15	AA065418	Primer to amplify
704	10.4	47.3	47	14	AAQ47803	Bilirubin oxidase	C	777	10.2	46.4	20	17	AA116094	Nia PCR primer NSX
705	10.4	47.3	47	14	AAQ47803	Bilirubin oxidase	C	778	10.2	46.4	20	17	AA116094	Nia PCR primer NSX
706	10.4	47.3	47	20	AAV72468	Human PRO533 clone	C	779	10.2	46.4	20	20	AA206117	PCR primer used to
707	10.4	47.3	47	21	AA266475	Human map-related	C	780	10.2	46.4	20	20	AA206117	PCR primer used to
708	10.4	47.3	47	21	AA266475	Human map-related	C	781	10.2	46.4	20	20	AA204089	PCR primer used to
709	10.4	47.3	47	21	AA267489	Human map-related	C	782	10.2	46.4	20	20	AA204089	PCR primer used to
710	10.4	47.3	47	21	AA267489	Human map-related	C	783	10.2	46.4	20	20	AA204089	PCR primer used to
711	10.4	47.3	48	16	AA086156	Sindbis primer SP6	C	784	10.2	46.4	20	20	AA203184	PCR primer used to
712	10.4	47.3	48	16	AA086156	Sindbis primer SP6	C	785	10.2	46.4	20	20	AA203184	PCR primer used to
713	10.4	47.3	48	17	AA135055	Sindbis virus geno	C	786	10.2	46.4	20	20	AA203184	PCR primer used to
714	10.4	47.3	48	17	AA135055	Sindbis virus geno	C	787	10.2	46.4	20	22	AA660154	Human ATM gene exo
715	10.4	47.3	48	17	AA135055	Sindbis virus geno	C	788	10.2	46.4	20	22	AA660154	Human ATM gene exo
716	10.4	47.3	48	17	AA130790	Sindbis genomic cd	C	789	10.2	46.4	20	24	ABK70814	Human TSP1 domain
717	10.4	47.3	48	18	AA130790	Sindbis genomic cd	C	790	10.2	46.4	20	24	ABK70814	Human TSP1 domain
718	10.4	47.3	48	18	AA130790	Sindbis genomic cd	C	791	10.2	46.4	20	24	ABK70814	PCR primer used to
719	10.4	47.3	48	19	AAV60128	PCR primer SP6-1A	C	792	10.2	46.4	20	24	ABK70814	PCR primer used to
720	10.4	47.3	48	19	AAV60128	PCR primer SP6-1A	C	793	10.2	46.4	20	24	ABK70814	Capture oligonucle
721	10.4	47.3	48	19	AAV42367	PCR primer SP6-1A	C	794	10.2	46.4	20	24	AB194036	Capture oligonucle
722	10.4	47.3	48	19	AAV42367	PCR primer SP6-1A	C	795	10.2	46.4	20	24	AB194036	Capture oligonucle
723	10.4	47.3	48	20	AA358483	Primer SP6-1A used	C	796	10.2	46.4	20	24	AB197193	Capture oligonucle
724	10.4	47.3	48	20	AA358483	Primer SP6-1A used	C	797	10.2	46.4	20	24	AB197193	Capture oligonucle
725	10.4	47.3	48	20	AA358483	Primer SP6-1A used	C	798	10.2	46.4	21	13	AA032568	HCV NS4-NS5 primer
726	10.4	47.3	48	20	AA352514	PCR primer for in	C	799	10.2	46.4	21	13	AA032568	HCV NS4-NS5 primer
727	10.4	47.3	48	20	AA352514	PCR primer for in	C	800	10.2	46.4	21	14	AA048540	HPV E6/7 region pr
728	10.4	47.3	48	20	AA352514	PCR primer for in	C	801	10.2	46.4	21	14	AA048540	HPV E6/7 region pr
729	10.4	47.3	48	20	AAV70687	EGF-like/FGF-8 hom	C	802	10.2	46.4	21	14	AA048544	HPV E6/7 region pr
730	10.4	47.3	48	20	AAV70687	EGF-like/FGF-8 hom	C	803	10.2	46.4	21	14	AA048544	HPV E6/7 region pr
731	10.4	47.3	48	21	AA358558	PCR primer SP6-1A	C	804	10.2	46.4	21	19	AA225833	Human polymorphic
732	10.4	47.3	48	21	AA358558	PCR primer SP6-1A	C	805	10.2	46.4	21	19	AA225833	Human polymorphic
733	10.4	47.3	48	21	AA358558	PCR primer SP6-1A	C	806	10.2	46.4	21	19	AA225833	Human polymorphic
734	10.4	47.3	48	21	AAA30097	Oligomer A-251H us	C	807	10.2	46.4	21	24	ABK83411	Polymerase express
735	10.4	47.3	48	21	AAA30097	Oligomer A-251H us	C	808	10.2	46.4	21	24	ABK83411	Polymerase express
736	10.4	47.3	48	21	AA289316	HPV 16 ori DNA fra	C	809	10.2	46.4	21	24	ABK83412	Polymerase express
737	10.4	47.3	48	21	AA289316	HPV 16 ori DNA fra	C	810	10.2	46.4	21	24	ABK83412	Polymerase express
738	10.4	47.3	48	21	AA292768	Sindbis virus geno	C	811	10.2	46.4	22	21	AA668654	NT3-Fab antibody f
739	10.4	47.3	48	21	AA292895	Sindbis virus geno	C	812	10.2	46.4	22	21	AA668654	NT3-Fab antibody f

C 813	10.2	46.4	22	22	AAF98756	Human IFN-alpha im	C 886	10.2	46.4	30	15	AAO70653	PCR primer BAMLINK
C 814	10.2	46.4	22	22	AAF98756	Human IFN-alpha im	C 887	10.2	46.4	30	17	AAI38777	SRV-1 primer 1 for
C 815	10.2	46.4	22	22	AAF99770	Immunostimulatory	C 888	10.2	46.4	30	17	AAI38777	SRV-1 primer 1 for
C 816	10.2	46.4	22	22	AAF99770	Immunostimulatory	C 889	10.2	46.4	30	20	AAV99980	Nucleotide sequenc
C 817	10.2	46.4	22	22	AAF99839	Immunostimulatory	C 890	10.2	46.4	30	20	AAV99980	Nucleotide sequenc
C 818	10.2	46.4	22	22	AAF99839	Immunostimulatory	C 891	10.2	46.4	30	22	AAA91591	PCR primer for S.
C 819	10.2	46.4	23	19	AAO99882	Human biallelic po	C 892	10.2	46.4	30	22	AAA91591	PCR primer for S.
C 820	10.2	46.4	23	19	AAO99882	Human biallelic po	C 893	10.2	46.4	30	22	AAA91591	PCR primer for S.
C 821	10.2	46.4	23	19	AAV61032	Plant embryo-speci	C 894	10.2	46.4	30	22	AAA37872	Temamyl-1-like alph
C 822	10.2	46.4	23	19	AAV61032	Plant embryo-speci	C 895	10.2	46.4	30	22	AAA37872	Temamyl-1-like alph
C 823	10.2	46.4	23	20	AAV84529	PCR primer for p90	C 896	10.2	46.4	30	24	ABK70816	Human TSPI domain
C 824	10.2	46.4	23	20	AAV84529	PCR primer for p90	C 897	10.2	46.4	31	22	AAI29920	Human single nucle
C 825	10.2	46.4	23	21	AAZ45845	PCR primer used am	C 898	10.2	46.4	31	22	AAI29920	Human single nucle
C 826	10.2	46.4	23	21	AAZ45845	PCR primer used am	C 899	10.2	46.4	31	22	AAI30199	Human single nucle
C 827	10.2	46.4	23	22	AAI65921	PCR primer #3, use	C 900	10.2	46.4	31	22	AAI30199	Human single nucle
C 828	10.2	46.4	23	22	AAI65921	PCR primer #3, use	C 901	10.2	46.4	32	21	AAA63981	PCR primer used to
C 829	10.2	46.4	24	10	AAV91579	Probe 1 for the de	C 902	10.2	46.4	32	21	AAA63981	PCR primer used to
C 830	10.2	46.4	24	10	AAV91579	Probe 1 for the de	C 903	10.2	46.4	32	21	AAZ49811	Primer Alex2 used
C 831	10.2	46.4	24	10	AAV93011	Probe for detectin	C 904	10.2	46.4	32	21	AAZ49811	Primer Alex2 used
C 832	10.2	46.4	24	10	AAV93011	Probe for detectin	C 905	10.2	46.4	33	13	AAQ31153	Probe 122 for geno
C 833	10.2	46.4	24	16	AAQ76194	Degenerate "nested	C 906	10.2	46.4	33	13	AAQ31153	Probe 122 for geno
C 834	10.2	46.4	24	16	AAQ76194	Degenerate "nested	C 907	10.2	46.4	33	14	AAQ46459	Hepatitis C virus
C 835	10.2	46.4	24	20	AAV33754	DNA tandem nucleot	C 908	10.2	46.4	33	14	AAQ46459	Hepatitis C virus
C 836	10.2	46.4	24	20	AAV33754	DNA tandem nucleot	C 909	10.2	46.4	33	19	AAV07856	HCV.33.4 capture p
C 837	10.2	46.4	24	20	AAV33721	DNA tandem nucleot	C 910	10.2	46.4	33	19	AAV07856	HCV.33.4 capture p
C 838	10.2	46.4	24	20	AAV33721	DNA tandem nucleot	C 911	10.2	46.4	33	20	AAV83084	Capture probe HCV.
C 839	10.2	46.4	24	24	ABO91872	M. capsulatus ORF	C 912	10.2	46.4	33	20	AAV83084	Capture probe HCV.
C 840	10.2	46.4	24	24	ABO91872	M. capsulatus ORF	C 913	10.2	46.4	33	24	ABA04379	ATRRF3 PCR primer
C 841	10.2	46.4	24	24	ABI83394	Capture oligonucle	C 914	10.2	46.4	33	24	ABA04379	ATRRF3 PCR primer
C 842	10.2	46.4	24	24	ABI83394	Capture oligonucle	C 915	10.2	46.4	33	24	AAV38418	Primer K31C1 for p
C 843	10.2	46.4	24	24	ABI83395	Capture oligonucle	C 916	10.2	46.4	34	19	AAV38418	Primer K31C1 for p
C 844	10.2	46.4	24	24	ABI83395	Capture oligonucle	C 917	10.2	46.4	34	19	AAV38418	Primer K31C1 for p
C 845	10.2	46.4	24	24	ABI84502	Capture oligonucle	C 918	10.2	46.4	35	19	AAV45317	FvK forward primer
C 846	10.2	46.4	24	24	ABI84502	Capture oligonucle	C 919	10.2	46.4	35	19	AAV45317	FvK forward primer
C 847	10.2	46.4	24	24	ABI84503	Capture oligonucle	C 920	10.2	46.4	35	14	AAO48270	Vibrio alginolytic
C 848	10.2	46.4	24	24	ABI84503	Capture oligonucle	C 921	10.2	46.4	36	16	AAO48270	Vibrio alginolytic
C 849	10.2	46.4	24	24	ABI84542	Capture oligonucle	C 922	10.2	46.4	36	16	AAI55418	Human re1a hamme
C 850	10.2	46.4	24	24	ABI84542	Capture oligonucle	C 923	10.2	46.4	36	16	AAI55418	Human re1a hamme
C 851	10.2	46.4	24	24	ABI84643	Capture oligonucle	C 924	10.2	46.4	36	16	AAI57532	RSV N hammerhead
C 852	10.2	46.4	24	24	ABI84643	Capture oligonucle	C 925	10.2	46.4	36	16	AAI57532	RSV N hammerhead
C 853	10.2	46.4	24	24	ABI87530	Capture oligonucle	C 926	10.2	46.4	36	16	AAI57180	RSV IC hammerhead
C 854	10.2	46.4	24	24	ABI87530	Capture oligonucle	C 927	10.2	46.4	36	16	AAI57180	RSV IC hammerhead
C 855	10.2	46.4	24	24	ABI87531	Capture oligonucle	C 928	10.2	46.4	36	17	AAI49962	Human CERP HH ribo
C 856	10.2	46.4	24	24	ABI87531	Capture oligonucle	C 929	10.2	46.4	36	17	AAI49962	Human CERP HH ribo
C 857	10.2	46.4	24	24	ABI90956	Capture oligonucle	C 930	10.2	46.4	36	17	AAI49969	Human CERP HH ribo
C 858	10.2	46.4	24	24	ABI90956	Capture oligonucle	C 931	10.2	46.4	36	17	AAI49969	Human CERP HH ribo
C 859	10.2	46.4	24	24	ABI90957	Capture oligonucle	C 932	10.2	46.4	36	21	AAZ43136	PCR primer for C.
C 860	10.2	46.4	24	24	ABI90957	Capture oligonucle	C 933	10.2	46.4	36	21	AAZ43136	PCR primer for C.
C 861	10.2	46.4	24	24	ABI91662	Capture oligonucle	C 934	10.2	46.4	37	21	AAI72907	Human insulin-like
C 862	10.2	46.4	24	24	ABI91662	Capture oligonucle	C 935	10.2	46.4	37	21	AAI72907	Human insulin-like
C 863	10.2	46.4	24	24	ABI91663	Capture oligonucle	C 936	10.2	46.4	37	21	AAI72910	Human insulin-like
C 864	10.2	46.4	24	24	ABI91663	Capture oligonucle	C 937	10.2	46.4	37	22	AAH49869	Bacterial 23S/5S R
C 865	10.2	46.4	26	24	ABK71095	Mouse HYPLIP1 locu	C 938	10.2	46.4	37	22	AAH49869	Bacterial 23S/5S R
C 866	10.2	46.4	26	24	ABK71095	Mouse HYPLIP1 locu	C 939	10.2	46.4	37	22	AAH49869	Bacterial 23S/5S R
C 867	10.2	46.4	26	24	ABK68191	Mouse HYPLIP1 locu	C 940	10.2	46.4	37	24	ABA95454	Human MHC class I
C 868	10.2	46.4	26	24	ABK68191	Mouse HYPLIP1 locu	C 941	10.2	46.4	37	24	ABA95454	Human MHC class I
C 869	10.2	46.4	27	18	AAV96353	Variable light cha	C 942	10.2	46.4	37	24	ABA95558	Human IGF-1 PCR pr
C 870	10.2	46.4	27	18	AAV96353	Variable light cha	C 943	10.2	46.4	38	15	AAO73036	Tyrosine-kinase sy
C 871	10.2	46.4	28	13	AAQ32727	Mouse light chain	C 944	10.2	46.4	38	15	AAO73036	Tyrosine-kinase sy
C 872	10.2	46.4	28	13	AAQ32727	Mouse light chain	C 945	10.2	46.4	38	15	AAO73037	Tyrosine-kinase sy
C 873	10.2	46.4	28	22	AAF82008	1.0 kb DNA fragmen	C 946	10.2	46.4	38	15	AAO73037	Tyrosine-kinase sy
C 874	10.2	46.4	28	22	AAF82008	1.0 kb DNA fragmen	C 947	10.2	46.4	38	18	AAI51264	Human AD4 gene gen
C 875	10.2	46.4	28	22	AAF82865	tpia gene PCR prim	C 948	10.2	46.4	38	18	AAI51264	Human AD4 gene gen
C 876	10.2	46.4	28	22	AAF82865	tpia gene PCR prim	C 949	10.2	46.4	38	22	AAH42703	PCR primer used to
C 877	10.2	46.4	28	24	ABJ55961	Mouse light chain	C 950	10.2	46.4	38	22	AAH42703	PCR primer used to
C 878	10.2	46.4	28	24	ABJ55961	Mouse light chain	C 951	10.2	46.4	38	22	AAH42703	PCR primer used to
C 879	10.2	46.4	29	19	AAV46267	Human corticostatin	C 952	10.2	46.4	38	22	AAH42703	PCR primer used to
C 880	10.2	46.4	29	19	AAV46267	Human corticostatin	C 953	10.2	46.4	38	22	AAH42703	PCR primer used to
C 881	10.2	46.4	29	21	AAO40380	Polymorphic fragme	C 954	10.2	46.4	38	23	ABK04311	Human NOGO Hamme
C 882	10.2	46.4	29	21	AAO40380	Polymorphic fragme	C 955	10.2	46.4	38	23	ABK04311	Human NOGO Hamme
C 883	10.2	46.4	30	10	AAV91936	Variable portion o	C 956	10.2	46.4	38	24	ABK57867	Human CLCA1 gene e
C 884	10.2	46.4	30	10	AAV91936	Variable portion o	C 957	10.2	46.4	38	24	ABK57867	Human CLCA1 gene e
C 885	10.2	46.4	30	15	AAO70653	PCR primer BAMLINK	C 958	10.2	46.4	38	24	ABK58916	Human CLCA1 gene e

ALIGNMENTS

XX	MO9845468-A1.
PD	15-OCT-1998.
XX	
PF	07-APR-1998; 98WO-USO6826.
XX	
PR	08-APR-1997; 97US-0043205.
XX	
PA	(USAS) NASA US NAT AERO & SPACE ADMIN.
PA	(TULA) TULANE EDUCATIONAL FUND.
PI	Goodwin TJ, Hammond TG, Kaysen JH;
XX	
DR	WPI; 1998-594488/50.
XX	
PT	Production of functional proteins - by culturing cells under microgravity conditions, and inducing gene expression with oligonucleotide directed against shear stress response element
XX	
PS	Example 16; Fig 4A; 55pp; English.
CC	The present sequence represents an antisense probe for the shear stress element. The probe has two possible conformations. As a singular strand it can fold back on itself to form a binding element for the transcription factor. As a double strand, it has two binding sites for the transcription factor (both in the sense and antisense orientation). The specification describes the expression of at least 1 gene which is induced in a cell by treating with a transcription factor decoy oligonucleotide directed against a sequence encoding a shear stress response element (SSRE). The method is used to produce hormones, toxin receptors and shear stress-dependent molecules, e.g., erythropoietin (EPO) for treatment of anaemia in dialysis or AIDS patients, and many forms of cancer. Also cells expressing these molecules are useful for biochemical, toxicological or pharmacological studies or as hormone implants.
CC	
CC	
SC	Sequence 22 BP; 5 A; 6 C; 6 G; 5 T; 0 other;
XX	
QY	Query Match 100.0%; Score 22; DB 19; Length 22; Best Local Similarity 100.0%; Pred. No. 0.088; Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB	1 CTGAGACCGATTCGCTCAG 22 1 CTGAGACCGATTCGCTCAG 22
RESULT 2	
AAV70907/C	
ID	AAV70907 standard; DNA; 22 BP.
XX	
AC	AAV70907;
XX	
DT	05-FEB-1999 (first entry)
DE	Antisense probe for shear stress response element.
XX	
KM	Antisense probe; shear response element; erythropoietin; anaemia; transcription factor decoy oligonucleotide; dialysis; AIDS; cancer; hormone implant; ss.
KW	
XX	
OS	Synthetic.
XX	
Key	Location/Qualifiers
FT	1..22
FT	/+tag= a
FT	misc_structure 1..9
FT	/+tag= b
FT	/note= "hybridises with nucleotides 14 to 22"
FT	14..22
FT	/+tag= c
FT	/note= "hybridises with nucleotides 1 to 9"
XX	

PN -MO9845468-A1.
XX
PD 15-OCT-1998.
XX
PF 07-APR-1998; 98WO-US066826.
XX
PR 08-APR-1997; 97US-0043205.
XX
PA (USAS) NASA US NAT AERO & SPACE ADMIN.
PA (TULA) TULANE EDUCATIONAL FUND.
XX
PI Goodwin TJ, Hammond TG, Kaysen JH;
XX
DR WPI; 1998-594468/50.
XX
PT Production of functional proteins - by culturing cells under
PT microgravity conditions, and inducing gene expression with
PT oligonucleotide directed against shear stress response element
XX
PS Example 16; Fig 4A; 55pp; English.
XX
CC The present sequence represents an antisense probe for the shear
CC response element. The probe has two possible conformations. As a singular
CC strand it can fold back on itself to form a binding element for the
CC transcription factor. As a double strand, it has two binding sites for
CC the transcription factor (both in the sense and antisense orientation).
CC The specification describes the expression of at least 1 gene which
CC is induced in a cell by treating with a transcription factor decoy
CC oligonucleotide directed against a sequence encoding a shear stress
CC response element (SSRE). The method is used to produce hormones, toxin
CC receptors and shear stress-dependent molecules, e.g. erythropoietin
CC (EPO) for treatment of anaemia in dialysis or AIDS patients, and many
CC forms of cancer. Also cells expressing these molecules are useful for
CC biochemical, toxicological or pharmacological studies or as hormone
CC implants.
XX
SQ Sequence 22 BP; 5 A; 6 C; 6 G; 5 T; 0 other;
XX
Query Match 100.0%; Score 22; DB 19; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.088;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGAGACCGATATCGGTCTCAG 22
Db 22 CTGAGACCGATATCGGTCTCAG 1
XX
RESULT 3
AAA70834
ID AAA70834 standard; RNA; 28 BP.
XX
AC AAA70834;
XX
DT 27-APR-2001 (first entry)
XX
DE Molecular interaction site RNA #34.
XX
KM Modulator; identification; molecular interaction; virtual library; ss.
XX
OS Mus sp.
XX
PN WO958947-A2.
XX
PD 18-NOV-1999.
XX
PF 12-MAY-1999; 99WO-US10361.
XX
PR 12-MAY-1998; 98US-0076404.
PR 12-MAY-1998; 98US-0085092.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;

PI Hofstadler S, McNeil J;
XX
DR WPI; 2000-086439/07.
XX
PT Identifying compounds which modulate activity of target biomolecules.
PT used to provide compounds which can be used as pharmacological,
PT agricultural and industrial compounds -
XX
PS Claim 275; Page 238; 405pp; English.
XX
CC This invention describes a novel method for identifying compounds which
CC modulate the activity of a target biomolecule. The method uses
CC 3-dimensional representations of the biomolecule and a library of
CC compounds and comprises (a) identifying at least one molecular
CC interaction site of the target RNA; (b) generating in silico a virtual
CC library of compounds predicted or calculated to interact with the
CC molecular interaction site; and (c) comparing 3-dimensional (3-D)
CC representations of the target RNA with members of the virtual library of
CC compounds to generate a hierarchy of the compounds ranked in accordance
CC with their respective ability to form physical interactions with the
CC molecular interaction site. The method also describes (1) RNA comprising
CC a joined sequence of at least 24 nucleotides but not more than 70
CC nucleotides and having secondary structure defined by: (a) 3 nucleotides
CC forming a first side of a first double stranded (ds) region; (b) 2
CC nucleotides forming a first side of an internal loop region; (c) 4
CC nucleotides forming a first side of a second ds region; (d) 4 or 5
CC nucleotides forming an end loop region; (e) 4 nucleotides forming a
CC second side of the second ds region; (f) 4 nucleotides forming a second
CC side of the internal loop region; and (g) 3 nucleotides forming a second
CC side of the first ds region; (2) a purified and isolated RNA fragment
CC comprising the human sequence UUUACACUAUUCUGUUCAGAAAUUC (11). The
CC methods and products can be used for identifying agents which modulate
CC the activity of biomolecules, particularly RNA. Such agents can be used
CC as pharmaceutical, agricultural or industrial compounds.
XX
SQ Sequence 28 BP; 11 A; 8 C; 4 G; 5 U; 0 other;
XX
Query Match 64.5%; Score 14.2; DB 21; Length 28;
Best Local Similarity 68.4%; Pred. No.: 9.2e+02;
Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 3 GAGACCGATATCGGTCTCA 21
Db 1 GAGACCGAAUUCUGUUCU 19
XX
RESULT 4
AAA70834/c
ID AAA70834 standard; RNA; 28 BP.
XX
AC AAA70834;
XX
DT 27-APR-2001 (first entry)
XX
DE Molecular interaction site RNA #34.
XX
KM Modulator; identification; molecular interaction; virtual library; ss.
XX
OS Mus sp.
XX
PN WO958947-A2.
XX
PD 18-NOV-1999.
XX
PF 12-MAY-1999; 99WO-US10361.
XX
PR 12-MAY-1998; 98US-0076404.
PR 12-MAY-1998; 98US-0085092.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
PI Hofstadler S, McNeil J;

XX WP1; 2000-086439/07.
XX
XX Identifying compounds which modulate activity of target biomolecules,
PT used to provide compounds which can be used as pharmacological,
PT agricultural and industrial compounds -
XX
PS Claim 275; Page 238; 405pp; English.
XX
CC This invention describes a novel method for identifying compounds which
CC modulate the activity of a target biomolecule. The method uses
CC 3-dimensional representations of the biomolecule and a library of
CC compounds and comprises (a) identifying at least one molecular
CC interaction site of the target RNA; (b) generating in silico a virtual
CC library of compounds predicted or calculated to interact with the
CC molecular interaction site; and (c) comparing 3-dimensional (3-D)
CC representations of the target RNA with members of the virtual library of
CC compounds to generate a hierarchy of the compounds ranked in accordance
CC with their respective ability to form physical interactions with the
CC molecular interaction site. The method also describes (1) RNA comprising
CC a joined sequence of at least 24 nucleotides but not more than 70
CC nucleotides and having secondary structure defined by: (a) 3 nucleotides
CC forming a first side of a first double stranded (ds) region; (b) 2
CC nucleotides forming a first side of an internal loop region; (c) 4
CC nucleotides forming a first side of a second ds region; (d) 4 or 5
CC nucleotides forming an end loop region; (e) 4 nucleotides forming a
CC second side of the second ds region; (f) 4 nucleotides forming a second
CC side of the internal loop region; and (g) 3 nucleotides forming a second
CC side of the first ds region; (2) a purified and isolated RNA fragment
CC comprising the human sequence UUUACAACAUAAUUCAGUUAACAAAUAUC (11). The
CC methods and products can be used for identifying agents which modulate
CC the activity of biomolecules, particularly RNA. Such agents can be used
CC as pharmaceutical, agricultural or industrial compounds.
XX
SQ Sequence 28 BP, 11 A; 8 C; 4 G; 5 U; 0 other;
Query Match 64.5%; Score 14.2; DB 21; Length 28;
Best Local Similarity 84.2%; Pred. NO. 9.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0.
DY 2 TGAGACCGATATCGGTCTC 20
Db 19 TGAGACAGATTGGGTCTC 1
RESULT 5
ID ABA98894 standard; DNA; 33 BP.
XX ABA98894;
XX AC
XX DT 07-MAY-2002 (first entry)
XX DE DNA sequence 2 relative to the farnesyltransferase of the invention.
XX KM Farnesyltransferase; enzyme; ds.
XX OS Unidentified.
XX KR98075770-A.
XX PD 16-NOV-1998.
XX PF 01-APR-1997; 97KR-0012067.
XX PR 01-APR-1997; 97KR-0012067.
XX PA (GDS) LG CHEM LTD.
XX PI Moon GD, Kim MJ, Chung HH;
XX WP1; 2000-020309/02.
XX

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PT Farnesyltransferase having histidine tag and process for preparing the
XX same.
XX
XX Disclosure; Page 9; 23pp; Korean.
XX
XX The invention relates to a farnesyltransferase with a histidine tag,
CC and methods for preparing it. The current sequence represents DNA
CC sequence 2 relative to the farnesyltransferase of the invention.
XX
XX
SQ Sequence 33 BP; 8 A; 8 C; 12 G; 5 T; 0 other;

Query Match 63.6%; Score 14; DB 21; Length 33;
Best Local Similarity 77.3%; Pred. No. 1.2e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 CTGAGACCGATATCGTCTCAG 22
   ||| ||||| ||||| |||
Db 2 CCGGATCGATATCGTACGAG 23

RESULT 6
ABA98894/C
ID ABA98894 standard; DNA; 33 BP.
XX
XX ABA98894;
XX
XX 07-MAY-2002 (first entry)
XX
XX DNA sequence 2 relative to the farnesyltransferase of the invention.
XX
XX Farnesyltransferase; enzyme; ds.
XX
XX Unidentified.
XX
XX KR98075770-A.
XX
XX 16-NOV-1998.
XX
XX 01-APR-1997; 97KR-0012067.
XX
XX 01-APR-1997; 97KR-0012067.
XX
XX (GLDS ) LG CHEM LTD.
XX
XX Moon GD, Kim MU, Chung HH;
XX
XX WPI; 2000-020309/02.
XX
XX Farnesyltransferase having histidine tag and process for preparing the
PT same.
XX
XX Disclosure; Page 9; 23pp; Korean.
XX
XX The invention relates to a farnesyltransferase with a histidine tag,
CC and methods for preparing it. The current sequence represents DNA
CC sequence 2 relative to the farnesyltransferase of the invention.
XX
XX
SQ Sequence 33 BP; 8 A; 8 C; 12 G; 5 T; 0 other;

Query Match 63.6%; Score 14; DB 21; Length 33;
Best Local Similarity 77.3%; Pred. No. 1.2e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 CTGAGACCGATATCGTCTCAG 22
   ||| ||||| ||||| |||
Db 23 CTGCTACCGATATCGATCCGG 2

RESULT 7
AA295872
ID AA295872 standard; DNA; 40 BP.
XX
XX AA295872;
XX

```

XX 10-APR-2000 (first entry)
 DT Polynucleotide sequence including binding site for BamHI.
 XX
 DE Ligand binding; restriction enzyme; nucleic acid determination;
 KW pharmaceutical; BamHI; ss.
 XX
 OS Synthetic.
 XX
 PN MO9963077-A2.
 XX
 PD 09-DEC-1999.
 XX
 PF 04-JUN-1999; 99WO-US12516.
 XX
 PR 04-JUN-1998; 98US-0087905.
 XX
 PR 03-JUN-1999; 99US-0324672.
 XX
 PA (TMTE-) TM TECHNOLOGIES INC.
 XX
 PI Lane MJ, Benight AS, Faldasz BD;
 XX
 DR WPI; 2000-116369/10.
 XX
 PT Modulating polynucleotide ligand binding site affinity using
 XX determination of the flanking duplex sequences -
 XX
 PS Example 1; Page 38; 62pp; English.
 XX
 CC The invention provides a method for determining the sequence of
 CC polynucleotide flanking regions that modulate ligand binding
 CC characteristics of an adjacent binding site. The method comprises:
 CC (i) providing a number of different duplex polynucleotides, each having
 CC the same polynucleotide ligand binding site and a randomly synthesised
 CC sequence flanking the binding site; (ii) exposing the duplex to a ligand
 CC selective for the binding site; (iii) isolating duplexes which bind or
 CC do not bind the ligand, and (iv) determining the nucleotide composition
 CC of the flanking duplex sequence by sequencing the duplex sequence
 CC adjacent to the binding site. The invention is used to modulate the
 CC ligand-binding characteristics of any nucleotide sequence. The invention
 CC is less costly and more efficient than prior art techniques that moderate
 CC ligand binding using small molecule pharmaceuticals. Sequences
 CC AA99762-296170 represent polynucleotide sequences including the binding
 CC site for the restriction enzyme BamHI and used in the course of the
 CC invention.
 XX
 SQ Sequence 40 BP; 8 A; 12 C; 13 G; 7 T; 0 other;
 XX
 Query Match 63.6%; Score 14; DB 21; Length 40;
 Best Local Similarity 77.3%; Pred. No. 1.2e+03;
 Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 XX
 QY 1 CTGAGACCGATATCGGCTTCAG 22
 DB 12 CAGAAACCGAGTTCGGCTTCAG 33
 XX
 RESULT 8
 AA95872/c
 ID AA95872 standard; DNA; 40 BP.
 XX
 AC AA95872;
 XX
 DT 10-APR-2000 (first entry)
 XX
 DE Polynucleotide sequence including binding site for BamHI.
 XX
 KW Ligand binding; restriction enzyme; nucleic acid determination;
 KW pharmaceutical; BamHI; ss.
 XX
 OS Synthetic.
 XX

PN MO9963077-A2.
 XX
 PD 09-DEC-1999.
 XX
 PF 04-JUN-1999; 99WO-US12516.
 XX
 PR 04-JUN-1998; 98US-0087905.
 XX
 PR 03-JUN-1999; 99US-0324672.
 XX
 PA (TMTE-) TM TECHNOLOGIES INC.
 XX
 PI Lane MJ, Benight AS, Faldasz BD;
 XX
 DR WPI; 2000-116369/10.
 XX
 PT Modulating polynucleotide ligand binding site affinity using
 XX determination of the flanking duplex sequences -
 XX
 PS Example 1; Page 38; 62pp; English.
 XX
 CC The invention provides a method for determining the sequence of
 CC polynucleotide flanking regions that modulate ligand binding
 CC characteristics of an adjacent binding site. The method comprises:
 CC (i) providing a number of different duplex polynucleotides, each having
 CC the same polynucleotide ligand binding site and a randomly synthesised
 CC sequence flanking the binding site; (ii) exposing the duplex to a ligand
 CC selective for the binding site; (iii) isolating duplexes which bind or
 CC do not bind the ligand, and (iv) determining the nucleotide composition
 CC of the flanking duplex sequence by sequencing the duplex sequence
 CC adjacent to the binding site. The invention is used to modulate the
 CC ligand-binding characteristics of any nucleotide sequence. The invention
 CC is less costly and more efficient than prior art techniques that moderate
 CC ligand binding using small molecule pharmaceuticals. Sequences
 CC AA99762-296170 represent polynucleotide sequences including the binding
 CC site for the restriction enzyme BamHI and used in the course of the
 CC invention.
 XX
 SQ Sequence 40 BP; 8 A; 12 C; 13 G; 7 T; 0 other;
 XX
 Query Match 63.6%; Score 14; DB 21; Length 40;
 Best Local Similarity 77.3%; Pred. No. 1.2e+03;
 Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 XX
 QY 1 CTGAGACCGATATCGGCTTCAG 22
 DB 33 CTGAGCCGAACTCGGTTCTG 12
 XX
 RESULT 9
 AAH46201
 ID AAH46201 standard; DNA; 33 BP.
 XX
 AC AAH46201;
 XX
 DT 21-SEP-2001 (first entry)
 XX
 DE Hexapetaloid duplicon-containing transferase 11 PCR primer. SEQ ID NO:6.
 XX
 KW Hexapetaloid duplicon-containing transferase 11; human;
 KW recombinant production; malignant tumour; cancer; blood disease;
 KW HIV infection; human immunodeficiency virus; immune disorder;
 KW inflammatory condition; cytostatic; anti-HIV; antiinflammatory;
 KW immunomodulator; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200148222-A1.
 XX
 PD 05-JUL-2001.
 XX
 PF 25-DEC-2000; 2000WO-CN00719.
 XX
 PR 27-DEC-1999; 99CN-0125376.
 XX

```

XX (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
XX
XX Mao Y, Xie Y;
XX WPI; 2001-418294/44.
XX
PT Hexapetaloid dupllicon containing transferase 11 and encoded
PT polynucleotide, applicable in diagnosis and treatment of malignant
PT tumor, hemopathy, HIV infection, immunological diseases and various
PT inflammation -
XX
XX Example 5; Page 18; 35pp; Chinese.
XX
CC The invention relates to human hexapetaloid dupllicon-containing
CC transferase 11 (AA897610), nucleic acids encoding it (AAH46197), and a
CC method for the recombinant production of hexapetaloid dupllicon-containing
CC transferase 11. The present invention additionally discloses an
CC antagonist of hexapetaloid dupllicon-containing transferase 11 for
CC therapeutic use, and an antibody which specifically binds to the protein.
CC Hexapetaloid dupllicon-containing transferase 11, and nucleotides which
CC encode it may be used for treating a variety of diseases, such as
CC malignant tumours, blood diseases, HIV (human immunodeficiency virus)
CC infection, immune disorders and inflammatory conditions. The protein may
CC also be used to screen for modulators of its activity or for peptide
CC fingerprinting identification. The polynucleotide can be used as a primer
CC for nucleic acid amplification reactions or as a probe for hybridisation
CC reactions, or in producing gene chips or microarrays. Sequences
CC AAH46200-AAH46201 represent PCR primers used in an exemplification of
CC the invention to amplify human hexapetaloid dupllicon-containing
CC transferase 11 cDNA for cloning.
XX
SQ Sequence 33 BP; 9 A; 8 C; 9 G; 7 T; 0 other;
XX
Query Match 61.8%; Score 13.6; DB 22; Length 33;
Best Local Similarity 80.0%; Pred. No. 1.9e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
OY 3 GAGACCGATATCGCTCTCAG 22
DB 14 GAGATCGATCATCTGAG 33
XX
RESULT 10
AAH46201/c
ID AAH46201 standard; DNA; 33 BP.
XX
AC AAH46201;
XX
DT 21-SEP-2001 (first entry)
XX
DE Hexapetaloid dupllicon-containing transferase 11 PCR primer, SEQ ID NO:6.
XX
XX Hexapetaloid dupllicon-containing transferase 11; human;
XX recombinant production; malignant tumour; cancer; blood disease;
XX HIV infection; human immunodeficiency virus; immune disorder;
XX inflammatory condition; cytostatic; anti-HIV; antiinflammatory;
XX immunomodulator; PCR primer; ss.
XX
XX Homo sapiens.
XX
XX WO200148222-A1.
XX
XX 05-JUL-2001.
XX
XX 25-DEC-2000; 2000WO-CN00719.
XX
XX 27-DEC-1999; 99CN-0125376.
XX
XX (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
XX
XX Mao Y, Xie Y;
XX
XX

```

```

DR WPI; 2001-418294/44.
XX
XX Hexapetaloid dupllicon containing transferase 11 and encoded
XX PT polynucleotide, applicable in diagnosis and treatment of malignant
XX PT tumor, hemopathy, HIV infection, immunological diseases and various
XX PT inflammation -
XX
XX Example 5; Page 18; 35pp; Chinese.
XX
CC The invention relates to human hexapetaloid dupllicon-containing
CC transferase 11 (AA897610), nucleic acids encoding it (AAH46197), and a
CC method for the recombinant production of hexapetaloid dupllicon-containing
CC transferase 11. The present invention additionally discloses an
CC antagonist of hexapetaloid dupllicon-containing transferase 11 for
CC therapeutic use, and an antibody which specifically binds to the protein.
CC Hexapetaloid dupllicon-containing transferase 11, and nucleotides which
CC encode it may be used for treating a variety of diseases, such as
CC malignant tumours, blood diseases, HIV (human immunodeficiency virus)
CC infection, immune disorders and inflammatory conditions. The protein may
CC also be used to screen for modulators of its activity or for peptide
CC fingerprinting identification. The polynucleotide can be used as a primer
CC for nucleic acid amplification reactions or as a probe for hybridisation
CC reactions, or in producing gene chips or microarrays. Sequences
CC AAH46200-AAH46201 represent PCR primers used in an exemplification of
CC the invention to amplify human hexapetaloid dupllicon-containing
CC transferase 11 cDNA for cloning.
XX
SQ Sequence 33 BP; 9 A; 8 C; 9 G; 7 T; 0 other;
XX
Query Match 61.8%; Score 13.6; DB 22; Length 33;
Best Local Similarity 80.0%; Pred. No. 1.9e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
OY 1 CTGAGACCGATATCGCTCTC 20
DB 33 CTCGAGCTGATCTCGATCTC 14
XX
RESULT 11
AB195602
ID AB195602 standard; DNA; 20 BP.
XX
AC AB195602;
XX
DT 16-FEB-2002 (first entry)
XX
DE Capture oligonucleotide zip ID#2689 oligo #9.
XX
XX Human; K-ras; PCR primer; probe; capture probe; mutation detection;
XX ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
XX infection; 21 hydroxylase deficiency; Turner Syndrome; obesity;
XX cancer; oncogene; tumour suppressor; human papillomavirus; forensic;
XX environmental monitoring; food industry; feed industry; ss.
XX
XX Synthetic.
XX
XX WO200179548-A2.
XX
XX 25-OCT-2001.
XX
XX 04-APR-2001; 2001WO-US10958.
XX
XX 14-APR-2000; 2000US-197271P.
XX
XX (CORR ) CORNELL RES FOUND INC.
XX
XX Barany F, Zivvi M, Gerry NP, Favis R, Klaman R;
XX
XX WPI; 2002-034366/04.
XX
XX Designing capture oligonucleotide probes for use on a support to which
XX complementary oligonucleotides hybridize with little mismatch -
XX
XX

```


PS Example 5; Fig 29; 300pp; English.
XX
CC The present invention describes a method (M1) for designing capture
CC oligonucleotide probes (I) for use on a support to which complementary
CC oligonucleotide probes (II) will hybridize with little mismatch, where
CC (I) have melting temperatures within a narrow range. The method is useful
CC for detecting infectious diseases caused by bacterial infectious agents
CC e.g. Salmonella, listeria monocytogenes and Haemophilus influenza, fungal
CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic citus,
CC Epstein-Barr virus and polio virus, and parasitic infectious agents,
CC selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
CC medialis. The method is also useful for detecting genetic diseases such
CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
CC involved in DNA amplification, replication, recombination or repair, the
CC cancer is specifically associated with a gene selected from BRCA1 gene,
CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
CC method is also used for environmental monitoring, forensics and the food
CC and feed industry, detecting comprises scanning (using e.g. a scanning
CC electron microscope and infrared microscope) the support at the
CC particular sites and identifying if ligation of the oligonucleotide probe
CC sets occurred and correlating (using a computer) identified ligation to a
CC presence or absence of the target nucleotide sequences. AB182074 to
CC AB197546 represent oligonucleotide sequences used in the exemplification
CC of the present invention.
XX
SQ Sequence 20 BP; 3 A; 7 C; 5 G; 5 T; 0 other;
XX
Query Match 60.9%; Score 13.4; DB 24; Length 20;
Best Local Similarity 93.3%; Pred. No. 2.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 8 CGATATCGTCTCAG 22
| | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | |
Db 5 CCGATATCGTCTCAG 19
XX
RESULT 12
AB195602/c
ID AB195602 standard; DNA; 20 BP.
XX
AC AB195602;
XX
DT 16-FEB-2002 (first entry)
XX
DE Capture oligonucleotide zip ID#2689 oligo #9.
XX
KW Human; K-ras; PCR primer; probe; capture probe; mutation detection;
KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity;
KW cancer; oncogene; tumour suppressor; human papillomavirus; forensic;
KW environmental monitoring; food industry; feed industry; ss.
XX
OS Synthetic.
XX
PN WO200179548-A2.
XX
PD 25-OCT-2001.
XX
PF 04-APR-2001; 2001WO-US10958.
XX
PR 14-APR-2000; 2000US-197271P.
XX
PA (CORR) CORNELL RES FOUND INC.
XX
PI Barany F, Zivvi M, Gerry NP, Favis R, Kliman R;
XX
DR WPI; 2002-034366/04.
XX
PT Designing capture oligonucleotide probes for use on a support to which
XX complementary oligonucleotides hybridize with little mismatch -

PS Example 5; Fig 29; 300pp; English.
XX
CC The present invention describes a method (M1) for designing capture
CC oligonucleotide probes (I) for use on a support to which complementary
CC oligonucleotide probes (II) will hybridize with little mismatch, where
CC (I) have melting temperatures within a narrow range. The method is useful
CC for detecting infectious diseases caused by bacterial infectious agents
CC e.g. Salmonella, listeria monocytogenes and Haemophilus influenza, fungal
CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic citus,
CC Epstein-Barr virus and polio virus, and parasitic infectious agents,
CC selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
CC medialis. The method is also useful for detecting genetic diseases such
CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
CC involved in DNA amplification, replication, recombination or repair, the
CC cancer is specifically associated with a gene selected from BRCA1 gene,
CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
CC method is also used for environmental monitoring, forensics and the food
CC and feed industry, detecting comprises scanning (using e.g. a scanning
CC electron microscope and infrared microscope) the support at the
CC particular sites and identifying if ligation of the oligonucleotide probe
CC sets occurred and correlating (using a computer) identified ligation to a
CC presence or absence of the target nucleotide sequences. AB182074 to
CC AB197546 represent oligonucleotide sequences used in the exemplification
CC of the present invention.
XX
SQ Sequence 20 BP; 3 A; 7 C; 5 G; 5 T; 0 other;
XX
Query Match 60.9%; Score 13.4; DB 24; Length 20;
Best Local Similarity 93.3%; Pred. No. 2.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1 CTGAGACCGATATCG 15
| | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | |
Db 19 CTGAGACCGATATCG 5
XX
RESULT 13
AB187774
ID AB187774 standard; DNA; 24 BP.
XX
AC AB187774;
XX
DT 15-FEB-2002 (first entry)
XX
DE Capture oligonucleotide zip ID#2689 oligo #1.
XX
KW Human; K-ras; PCR primer; probe; capture probe; mutation detection;
KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity;
KW cancer; oncogene; tumour suppressor; human papillomavirus; forensic;
KW environmental monitoring; food industry; feed industry; ss.
XX
OS Synthetic.
XX
PN WO200179548-A2.
XX
PD 25-OCT-2001.
XX
PF 04-APR-2001; 2001WO-US10958.
XX
PR 14-APR-2000; 2000US-197271P.
XX
PA (CORR) CORNELL RES FOUND INC.
XX
PI Barany F, Zivvi M, Gerry NP, Favis R, Kliman R;
XX
DR WPI; 2002-034366/04.
XX
PT Designing capture oligonucleotide probes for use on a support to which
XX complementary oligonucleotides hybridize with little mismatch -

PS Example 5; Fig 25; 300pp; English.
 XX
 CC The present invention describes a method (M1) for designing capture
 CC oligonucleotide probes (I) for use on a support to which complementary
 CC oligonucleotide probes (II) will hybridise with little mismatch, where
 CC (I) have melting temperatures within a narrow range. The method is useful
 CC for detecting infectious diseases caused by bacterial infectious agents
 CC e.g. Salmonella, listeria monocytogenes and Haemophilus influenza, fungal
 CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
 CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
 CC Epstein-Barr virus and polio virus, and parasitic infectious agents
 CC selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
 CC medialis. The method is also useful for detecting genetic diseases such
 CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
 CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
 CC involved in DNA amplification, replication, recombination or repair, the
 CC cancer is specifically associated with a gene selected from BRCA1 gene,
 CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
 CC method is also used for environmental monitoring, forensics and the food
 CC and feed industry, detecting comprises scanning (using e.g. a scanning
 CC electron microscope and infrared microscope) the support at the
 CC particular sites and identifying if ligation of the oligonucleotide probe
 CC sets occurred and correlating (using a computer) identified ligation to a
 CC presence or absence of the target nucleotide sequences. AB182074 to
 CC AB197546 represent oligonucleotide sequences used in the exemplification
 CC of the present invention.
 CC
 SO Sequence 24 BP; 7 A; 6 C; 8 G; 3 T; 0 other;
 Query Match 60.9%; Score 13.4; DB 24; Length 24;
 Best Local Similarity 93.3%; Pred. No. 2.3e+03;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CTGAGACCGGATATCG 15
 Db 6 CTGAGACCGGATATCG 20
 RESULT 16
 AB187775/C
 ID AB187775 standard; DNA; 24 BP.
 XX
 AC AB187775;
 XX
 DT 15-FEB-2002 (first entry)
 XX
 DE Capture oligonucleotide zip ID#2689 oligo #2.
 XX
 KW Human; K-ras; PCR primer; probe; capture probe; mutation detection;
 KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
 KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity;
 KW cancer; oncogene; tumour suppressor; human papillomavirus; forensic;
 KW environmental monitoring; food industry; feed industry; ss.
 XX
 OS Synthetic.
 XX
 PN WO200179548-A2.
 XX
 PD 25-OCT-2001.
 XX
 PF 04-APR-2001; 2001WO-US10958.
 XX
 PR 14-APR-2000; 2000US-197271P.
 XX
 PA (CORR) CORNELL RES FOUND INC.
 XX
 PI Barany F, Zivvi M, Gerry NP, Favys R, Kliman R;
 XX
 DR WPI; 2002-034366/04.
 XX
 PT Designing capture oligonucleotide probes for use on a support to which
 PT complementary oligonucleotides hybridize with little mismatch -
 XX

PS Example 5; Fig 25; 300pp; English.
 XX
 CC The present invention describes a method (M1) for designing capture
 CC oligonucleotide probes (I) for use on a support to which complementary
 CC oligonucleotide probes (II) will hybridise with little mismatch, where
 CC (I) have melting temperatures within a narrow range. The method is useful
 CC for detecting infectious diseases caused by bacterial infectious agents
 CC e.g. Salmonella, listeria monocytogenes and Haemophilus influenza, fungal
 CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
 CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
 CC Epstein-Barr virus and polio virus, and parasitic infectious agents
 CC selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
 CC medialis. The method is also useful for detecting genetic diseases such
 CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
 CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
 CC involved in DNA amplification, replication, recombination or repair, the
 CC cancer is specifically associated with a gene selected from BRCA1 gene,
 CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
 CC method is also used for environmental monitoring, forensics and the food
 CC and feed industry, detecting comprises scanning (using e.g. a scanning
 CC electron microscope and infrared microscope) the support at the
 CC particular sites and identifying if ligation of the oligonucleotide probe
 CC sets occurred and correlating (using a computer) identified ligation to a
 CC presence or absence of the target nucleotide sequences. AB182074 to
 CC AB197546 represent oligonucleotide sequences used in the exemplification
 CC of the present invention.
 CC
 SO Sequence 24 BP; 7 A; 6 C; 8 G; 3 T; 0 other;
 Query Match 60.9%; Score 13.4; DB 24; Length 24;
 Best Local Similarity 93.3%; Pred. No. 2.3e+03;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 8 CGATATCGGCTCTGAG 22
 Db 20 CGATATCGGCTCTGAG 6
 RESULT 17
 AAX04272
 ID AAX04272 standard; DNA; 36 BP.
 XX
 AC AAX04272;
 XX
 DT 15-APR-1999 (first entry)
 XX
 DE HAV-A linker regions of pAP-257.
 XX
 KW Ricin-like toxin; cancer; viral infection; parasitic infection;
 KW linker; B chain; A chain; protease; fungal infection; malaria;
 KW leucocyte proliferation; cytomegalovirus; herpes; hepatitis;
 KW rhinovirus; laryngeotracheitis; poliomyelitis; varicella zoster;
 KW cystic fibrosis; multiple sclerosis; ds.
 XX
 OS Hepatitis A virus.
 XX
 PN WO9849311-A2.
 XX
 PD 05-NOV-1998.
 XX
 PF 30-APR-1998; 98WO-CA00394.
 XX
 PR 29-OCT-1997; 97US-0063715.
 XX
 PR 30-APR-1997; 97US-0045148.
 XX
 PA (DNOV-) DE NOVO ENZYME CORP.
 XX
 PI Borgford T;
 XX
 DR WPI; 1999-009431/01.
 XX
 PT New nucleic acid encoding ricin-like toxin with an interchain linker
 PT

PT cleaved by protease - is specific for diseased cells, useful for,
 XX e.g. killing selectively cancer or infected cells
 PS Disclosure; Fig 23B; 352pp; English.

XX The present invention describes new purified and isolated nucleic acids
 CC (1) encoding: (i) the A and B chains of a ricin-like toxin (ii); and
 CC (ii) a heterologous linker, joining the two chains and including a
 CC cleavage recognition site for a disease-specific protease (iii). Also
 CC described are: (1) plasmids or baculovirus transfer vectors that contain
 CC (i); and (2) recombinant protein (iv) consisting of the A and B chains
 CC of (ii) joined by the specified linker. (iv), produced by expression of
 CC (i) in host cells, are used to inhibit or kill diseased cells that
 CC produce (iii), particularly for treating cancers (e.g. leucocyte
 CC proliferation; cancer of ovary, pancreas, breast or prostate; glioma) or
 CC infections caused by fungi, parasites (e.g. malaria) or viruses (e.g.
 CC cytomegalovirus (CMV), herpes, hepatitis, rhinovirus, laryngeotracheitis,
 CC poliomyelitis or varicella zoster), also cystic fibrosis and multiple
 CC sclerosis. Alternatively, (i) is used to express (iv) in vivo. (iv) is
 CC toxic specifically for (iii)-expressing cells and does not depend for
 CC specificity on a cell-binding component. When used to treat virus-
 CC infected cells, transcytosis and cytotoxicity of (iv) are increased by
 CC retrograde translocation from endoplasmic reticulum to cytoplasm (which
 CC some viruses exploit to avoid immune detection), so selectivity and
 CC safety are further improved. (iv) are not toxic until chain A is
 CC released and this occurs only in target cells. The present sequence
 CC represents a nucleotide sequence from the present invention.

XX Sequence 36 BP; 11 A; 7 C; 7 G; 11 T; 0 other;

Query Match 59.1%; Score 13; DB 20; Length 36;
 Best Local Similarity 76.2%; Pred. No. 3.9e+03;
 Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CTGAGACCGATATCGTCTCA 21
 |||||
 DB 7 CTTGAGACCGATATCGTCTCA 27

RESULT 18
 AAX04272/c
 ID AAX04272 standard; DNA; 36 BP.
 XX
 AC AAX04272;

DT 15-APR-1999 (first entry)

XX HAV-A linker regions of pap-257.

XX Ricin-like toxin; cancer; viral infection; parasitic infection;
 KM linker; B chain; A chain; protease; fungal infection; malaria;
 KM leucocyte proliferation; cytomegalovirus; herpes; hepatitis;
 KM rhinovirus; laryngeotracheitis; poliomyelitis; varicella zoster;
 KM cystic fibrosis; multiple sclerosis; ds.

XX Hepatitis A virus.
 OS Synthetic.

PN W09849311-A2.

PD 05-NOV-1998.

PF 30-APR-1998; 98WO-CA00394.

PR 29-OCT-1997; 97US-0063715.

PA 30-APR-1997; 97US-0045148.

XX (DNOV-) DE NOVO ENZYME CORP.

PI Borgford T;

XX WPI; 1999-009431/01.

PT New nucleic acid encoding ricin-like toxin with an interchain linker
 XX cleaved by protease - is specific for diseased cells, useful for,
 PT e.g. killing selectively cancer or infected cells
 PS Disclosure; Fig 23B; 352pp; English.

XX The present invention describes new purified and isolated nucleic acids
 CC (1) encoding: (i) the A and B chains of a ricin-like toxin (ii); and
 CC (ii) a heterologous linker, joining the two chains and including a
 CC cleavage recognition site for a disease-specific protease (iii). Also
 CC described are: (1) plasmids or baculovirus transfer vectors that contain
 CC (i); and (2) recombinant protein (iv) consisting of the A and B chains
 CC of (ii) joined by the specified linker. (iv), produced by expression of
 CC (i) in host cells, are used to inhibit or kill diseased cells that
 CC produce (iii), particularly for treating cancers (e.g. leucocyte
 CC proliferation; cancer of ovary, pancreas, breast or prostate; glioma) or
 CC infections caused by fungi, parasites (e.g. malaria) or viruses (e.g.
 CC cytomegalovirus (CMV), herpes, hepatitis, rhinovirus, laryngeotracheitis,
 CC poliomyelitis or varicella zoster), also cystic fibrosis and multiple
 CC sclerosis. Alternatively, (i) is used to express (iv) in vivo. (iv) is
 CC toxic specifically for (iii)-expressing cells and does not depend for
 CC specificity on a cell-binding component. When used to treat virus-
 CC infected cells, transcytosis and cytotoxicity of (iv) are increased by
 CC retrograde translocation from endoplasmic reticulum to cytoplasm (which
 CC some viruses exploit to avoid immune detection), so selectivity and
 CC safety are further improved. (iv) are not toxic until chain A is
 CC released and this occurs only in target cells. The present sequence
 CC represents a nucleotide sequence from the present invention.

XX Sequence 36 BP; 11 A; 7 C; 7 G; 11 T; 0 other;

Query Match 59.1%; Score 13; DB 20; Length 36;
 Best Local Similarity 76.2%; Pred. No. 3.9e+03;
 Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 TGAGACCGATATCGTCTCAG 22
 |||||
 DB 27 TGAGACCGATATCGTCTCAG 7

RESULT 19
 AAT78823
 ID AAT78823 standard; DNA; 44 BP.
 XX
 AC AAT78823;

DT 23-JUN-1998 (first entry)

XX Kappa light chain PCR reaction 2 PCR primer O-561.

XX Ig; affinity constant; human; antigen; hybridoma; B cell; transgene;
 KM transgenic; mouse; CD4; antibody; autoimmune; inflammatory;
 KM transplant rejection; immunoglobulin; ss.

XX Synthetic.

OS Homo sapiens.

PN W09713852-A1.

PD 17-APR-1997.

PF 10-OCT-1996; 96WO-US16433.

PR 10-OCT-1995; 95US-0544404.

XX (GENP-) GENPHARM INT INC.

PI Kay RM, Lonberg N;

XX WPI; 1997-235888/21.

XX Novel anti-CD4 antibody produced by transgenic mice - used in the
 PT treatment of auto-immune disease etc.

XX Example 42; Page 266; 396pp; English.
PS A novel composition has been developed which comprises an immunoglobulin
XX (Ig) having an affinity constant (Ka) of at least 2 multiply
CC 1000000000 M-1 for binding to a predetermined human antigen. The present
CC sequence represents a PCR primer involved in the light chain PCR
CC reaction 2 for the production of a synthetic kappa light chain. Anti-
CC CD4 antibodies may be used in therapeutic and diagnostic applications,
CC especially for the treatment of human diseases. These antibodies reduce
CC activity of CD4 cells and reduce undesirable autoimmune reactions,
CC inflammatory response and transplant rejection. Transgenic animals are
CC capable of producing heterologous antibodies of multiple isotypes by
CC undergoing isotype switching. These animals produce a first Ig type
CC that is necessary for antigen-stimulated B-cell maturation and can
CC switch to encode and produce one or more subsequent heterologous
CC isotypes.
SQ Sequence 44 BP; 10 A; 11 C; 12 G; 11 T; 0 other;
XX
XX
Query Match 59.1%; Score 13; DB 18; Length 44;
Best Local Similarity 76.2%; Pred. No. 3.9e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 2 TGAGACCGATATCGTCTCAG 22
Db 9 TGAGAGTGAATCTGTCCAG 29
RESULT 20
AAV78823/c
ID AAV78823 standard; DNA; 44 BP.
XX
XX AAT78823;
AC
XX 23-JAN-1998 (first entry)
DT
XX
XX
DE Kappa light chain PCR reaction 2 PCR primer O-561.
XX
XX Ig; affinity constant; human; antigen; hybridoma; B cell; transgene;
KW transgenic; mouse; CD4; antibody; autoimmune; inflammatory;
KW transplant rejection; immunoglobulin; ss.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX WO9713852-A1.
PN
XX 17-APR-1997.
PD
XX
XX 10-OCT-1996; 96WO-US16433.
PF
XX 10-OCT-1995; 95US-0544404.
PR
XX (GENP-) GENPHARM INT. INC.
PA
XX
XX Kay RM, Lonberg N;
PI
XX WPI; 1997-235888/21.
DR
XX
XX Novel anti-CD4 antibody produced by transgenic mice - used in the
PT treatment of auto-immune disease etc.
XX
XX
PS Example 42; Page 266; 396pp; English.
XX
XX A novel composition has been developed which comprises an immunoglobulin
CC (Ig) having an affinity constant (Ka) of at least 2 multiply
CC 1000000000 M-1 for binding to a predetermined human antigen. The present
CC sequence represents a PCR primer involved in the light chain PCR
CC reaction 2 for the production of a synthetic kappa light chain. Anti-
CC CD4 antibodies may be used in therapeutic and diagnostic applications,
CC especially for the treatment of human diseases. These antibodies reduce
CC activity of CD4 cells and reduce undesirable autoimmune reactions,

CC inflammatory response and transplant rejection. Transgenic animals are
CC capable of producing heterologous antibodies of multiple isotypes by
CC undergoing isotype switching. These animals produce a first Ig type
CC that is necessary for antigen-stimulated B-cell maturation and can
CC switch to encode and produce one or more subsequent heterologous
CC isotypes.
SQ Sequence 44 BP; 10 A; 11 C; 12 G; 11 T; 0 other;
XX
XX
Query Match 59.1%; Score 13; DB 18; Length 44;
Best Local Similarity 76.2%; Pred. No. 3.9e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 CTGAGACCGATATCGTCTCA 21
Db 29 CTGGACAGATTCTCACTCTCA 9
RESULT 21
AAV39264
ID AAV39264 standard; DNA; 44 BP.
XX
XX AAV39264;
AC
XX 18-DEC-1998 (first entry)
DT
XX
XX
DE Primer O-561 used to make a synthetic kappa light chain.
XX
XX Transgenic animal; human heterologous antibody; transgene;
KW isotype switching; neutrophil efflux; reperfusion injury; CD4 binding;
KW autoimmune reaction; inflammatory response; transplant rejection;
KW acid induced lung injury; acute adult respiratory distress syndrome;
KW ARDS; vasculitis; septic shock; allergic reaction; asthma;
KW cystic fibrosis; PCR primer; ss.
XX
XX Synthetic.
OS
XX
XX WO9824884-A1.
PN
XX 11-JUN-1998.
PD
XX
XX 01-DEC-1997; 97WO-US21803.
PF
XX 02-DEC-1996; 96US-0758417.
PR
XX (GENP-) GENPHARM INT.
PA
XX
XX Kay RM, Lonberg N;
PI
XX
XX WPI; 1998-333306/29.
DR
XX
XX Hybridoma producing antibody specific for interleukin-8 - used to
PT prevent efflux of neutrophils from vasculature, and treat
PT reperfusion injury
XX
XX
PS Example 42; Page 317; 452pp; English.
XX
XX Oligonucleotides AAV39256-64 were used to create a synthetic kappa light
CC chain. Oligonucleotides AAV39256-64 were pooled, and amplified with the
CC AAV39248 and AAV39265. The amplification product was combined with the
CC product of oligonucleotides AAV39244-53, and then amplified. The sequence
CC was then cloned into a vector, which is used to produce the transgenic
CC mouse of the invention. The specification describes transgenic non-human
CC animals, especially a mouse, which are capable of producing a human
CC heterologous antibodies of multiple isotypes by undergoing isotype
CC switching. The transgenic animals have human heavy and light chain
CC transgenes. The transgenes are capable of functionally rearranging a
CC heterologous diversity (D) gene in a variable-diversity-junction (V-D-J)
CC recombination. The transgenes include a heavy chain transgene comprising
CC at least one V, D and J gene segment, and one constant region gene
CC segment. The immunoglobulin (Ig) light chain transgene comprises at
CC least one V and J gene segment and one constant region gene segment. The
CC gene segments are heterologous to the transgenic animal. The antibody can

CC be used to prevent efflux of neutrophils from vasculature. It can also
CC be used to treat reperfusion injury. CD4 binding antibodies are used to
CC reduce undesirable autoimmune reactions, inflammatory responses and
CC rejection of transplanted organs. The anti-IL-8 antibodies can reduce
CC tissue damage and prolong survival in animal models of acute adult
CC respiratory distress syndrome (ARDS) and acid induced lung injury. The
CC anti-IL-8 antibodies can also be used for the treatment of vasculitis,
CC septic shock, allergic reactions (e.g. asthma) and cystic fibrosis.
XX
SQ Sequence 44 BP; 10 A; 11 C; 12 G; 11 T; 0 other;

Query Match 59.1%; Score 13; DB 19; Length 44;
Best Local Similarity 76.2%; Pred. No. 3.9e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 TGAGACCGATATCGGTCTCAG 22
DB 9 TGAGAGTGAATCTGTCCAG 29

RESULT 22

AAV39264/C
ID AAV39264 standard; DNA; 44 BP.

AC AAV39264;
XX
DT 18-DEC-1998 (first entry)

DE Primer 0-561 used to make a synthetic kappa light chain.

XX Transgenic animal; human heterologous antibody; transgene;
KM isotype switching; neutrophil efflux; reperfusion injury; CD4 binding;
KM autoimmune reaction; inflammatory response; transplant rejection;
KM acid induced lung injury; acute adult respiratory distress syndrome;
KM ARDS; vasculitis; septic shock; allergic reaction; asthma;
KM cystic fibrosis; PCR primer; ss.
XX
OS Synthetic.

PN WO9824884-A1.

PD 11-JUN-1998.

PF 01-DEC-1997; 97WO-US21803.

PR 02-DEC-1996; 96US-0758417.

XX (GENP-) GENPHARM INT.

PA Kay RM, Lonberg N;

XX WPI; 1998-333306/29.

DR Hybridoma producing antibody specific for interleukin-8 - used to
XX prevent efflux of neutrophils from vasculature, and treat
PT reperfusion injury
XX

PS Example 42; Page 317; 452pp; English.

XX Oligonucleotides AAV39256-64 were used to create a synthetic kappa light
CC chain. Oligonucleotides AAV39256-64 were pooled, and amplified with the
CC AAV39248 and AAV39265. The amplification product was combined with the
CC product of oligonucleotides AAV39244-53, and then amplified. The sequence
CC was then cloned into a vector, which is used to produce the transgenic
CC mouse of the invention. The specification describes transgenic non-human
CC animals, especially a mouse, which are capable of producing a human
CC heterologous antibodies of multiple isotypes by undergoing isotype
CC switching. The transgenic animals have human heavy and light chain
CC transgenes. The transgenes are capable of functionally rearranging a
CC heterologous diversity (D) gene in a variable-diversity-junction (V-D-J)
CC recombination. The transgenes include a heavy chain transgene comprising
CC at least one V, D and J gene segment, and one constant region gene
CC segment. The immunoglobulin (Ig) light chain transgene comprises at

CC least one V and J gene segment and one constant region gene segment. The
CC gene segments are heterologous to the transgenic animal. The antibody can
CC be used to prevent efflux of neutrophils from vasculature. It can also
CC be used to treat reperfusion injury. CD4 binding antibodies are used to
CC reduce undesirable autoimmune reactions, inflammatory responses and
CC rejection of transplanted organs. The anti-IL-8 antibodies can reduce
CC tissue damage and prolong survival in animal models of acute adult
CC respiratory distress syndrome (ARDS) and acid induced lung injury. The
CC anti-IL-8 antibodies can also be used for the treatment of vasculitis,
CC septic shock, allergic reactions (e.g. asthma) and cystic fibrosis.
XX
SQ Sequence 44 BP; 10 A; 11 C; 12 G; 11 T; 0 other;

Query Match 59.1%; Score 13; DB 19; Length 44;
Best Local Similarity 76.2%; Pred. No. 3.9e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CTGAGACCGATATCGGTCTCA 21
DB 29 CTGGAGAGATTCTCACTCA 9

RESULT 23

AAZ22018
ID AAZ22018 standard; DNA; 44 BP.

XX AAZ22018;

DT 24-NOV-1999 (first entry)

DE Oligonucleotide used for minigene construction.

XX Transgenic animal; heterologous antibody; hybridoma; B cell;
KM transgenic mouse; human heavy chain transgene; digoxin;
KM human light chain transgene; immortalized cell; immunoglobulin;
KM Shiga-like toxin; autoimmune disease; cancer; infectious disease;
KM transplant rejection; blood disorder; coagulation disorder; ss.
XX
OS Synthetic.

PN WO945962-A1.

PD 16-SEP-1999.

PF 12-MAR-1999; 99WO-US05535.

PR 13-MAR-1998; 98US-0042353.

XX (GENP-) GENPHARM INT INC.

PA Lonberg N, Fishwild DM, Ball WJ;

XX WPI; 1999-551219/46.

DR Novel transgenic non-human animals used to produce heterologous
XX antibodies
PT
XX

PS Example 42; Page 318; 484pp; English.

XX The specification describes transgenic animals that are capable of
CC producing a heterologous antibody. The antibodies are isolated from a
CC hybridoma, comprising B cells, that is obtained from a transgenic mouse
CC having a genome comprising a human heavy chain transgene and a human
CC light chain transgene. The B cells are fused to immortalized cells
CC suitable for generating a hybridoma, which produces a detectable
CC amount of an immunoglobulin that specifically binds digoxin or
CC Shiga-like toxin. B cells from transgenic animals can be used to
CC generate hybridomas expressing monoclonal high affinity human sequence
CC antibodies. Antibodies produced from the transgenic animals of the
CC invention can be used to treat human diseases, e.g. autoimmune
CC diseases, cancer, infectious disease, transplant rejection, blood
CC disorders such as coagulation disorders and other diseases. The
CC present sequence is used in the course of the invention.

XX Sequence 44 BP; 10 A; 11 C; 12 G; 11 T; 0 other;
SQ

Query Match	59.1%;	Score 13;	DB 20;	Length 44;
Best Local Similarity	76.2%;	Pred. No. 3.9e+03;		
Matches 16; Conservative	0;	Mismatches 5;	Indels 0;	Gaps 0;

```
QY      2 TGAGACCGATATCGGTCTCAG 22
          ||||| | ||||| |||||
Db      9 TGAGAGTGAATCTGTCCAG 29
```

RESULT 24
AAZ22018/c
ID AAZ22018 standard; DNA; 44 BP.

AC AAZ22018;

DT 24-NOV-1999 (first entry)

Oligonucleotide used for minigene construction.

KM Transgenic animal; heterologous antibody; hybridoma; B cell;
 KM transgenic mouse; human heavy chain transgene; digoxin;
 KM human light chain transgene; immortalized cell; immunoglobulin;
 KM Shingna-like toxin; autoimmune disease; cancer; infectious disease;
 KM transplant rejection; blood disorder; coagulation disorder; ss.

OS Synthetic.

PN W09945962-A1.

PD 16-SEP-1999

PF 12-MAR-1999; 99WO-US05535.

PR 13-MAR-1998; 98US-0042353.

PA (GENP-) GENPHARM INT INC.

PI Lonberg N, Fishwild DM, Ball WJ;
.....

DR WPI; 1999-551219/46.

PT. Novel transgenic non-human animals used to produce heterologous PT antibodies

PS Example 42; Page 318; 484pp; English.

The specification describes transgenic animals that are capable of producing a heterologous antibody. The antibodies are isolated from a hybridoma, comprising B cells, that is obtained from a transgenic mouse having a genome comprising a human heavy chain transgene and a human light chain transgene. The B cells are fused to immortalized cells suitable for generating a hybridoma, which produces a detectable amount of an immunoglobulin that specifically binds digoxin or Shiga-like toxin. B cells from transgenic animals can be used to generate hybridomas expressing monoclonal high affinity human sequence antibodies. Antibodies produced from the transgenic animals of the invention can be used to treat human diseases, e.g. autoimmune diseases, cancer, infectious disease, transplant rejection, blood disorders such as coagulation disorders and other diseases. The present sequence is used in the course of the invention.

SQ Sequence 44 BP; 10 A; 11 C; 12 G; 11 T; 0 other;

Query Match	59.1%;	Score 13;	DB 20;	Length 44;
Best Local Similarity	76.2%;	Pred. No. 3.9e+03;		
Matches 16;	Conservative 0;	Mismatches 5;	Indels 0;	Gaps 0;

Qy 1 CTGAGACCGATATCGGTCTCA 21
||| ||| ||| ||| |||
Db 29 CTGGACACAGATTTCACCTCTCA 9

RESULT 25

ID	AAZ43102 standard; DNA; 24 BP.
ref	

AC AAZ43102;

DT 04-FEB-2000 (first entry)

DE PCR primer for *C. elegans* insulin-like protein ZK84.6.

KW Insulin-like protein; diagnosis; insulin-like gene analysis; nematode;
KW insulin hormone; aging; senescence; pesticide target; signalling pathway;
KW signal transduction pathway; PCR primer; ss.

OS Synthetic.
OS Caenorhabditis elegans.

PN WO9954436-A2.

PD 28-OCT-1999.

PF 16-APR-1999; 99WO-US08522.

PR 17-APR-1998; 98US-0062580.

PR 26-MAY-1998; 98US-0084303.

PA (EXEL-) EXELIXIS PHARM INC.

PI Homburger SA, Platt DM, Fe

3 XX
4
5
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9
10
11
12

24 XX

PT acids and proteins c

PS Example 1; Page 45; 194pp; English.

This sentence represents a PCR primer for DNA encoding a Caenorhabditis elegans insulin-like protein. The amplified sequence can be used in the method of the invention, for analysing an effect of expression or mis-expression of a C. elegans insulin-like gene, which comprises observing a first nematode genetically engineered to express or mis-express a C. elegans insulin-like protein (ILP) of any one of groups I, II or IV or a derivative or fragment that displays one or more functional activities of the C. elegans ILP. The insulin-like genes in C. elegans constitute very useful tools for probing the function and regulation of their corresponding pathways. This can be expected to lead to the discovery of new drug targets, therapeutic proteins, diagnostics and prognostics useful in the treatment of diseases and clinical problems associated with the function of insulin hormones in humans and other animals, as well as clinical problems associated with aging and senescence. The information may also be useful in identification and validation of pesticide targets in invertebrate pests that are components of these signalling pathways. The genes are also useful for identifying factors that are upstream of the receptor in the signal transduction pathway. The ligand-encoding C. elegans insulin-like genes provide a superior approach for identifying factors that are upstream of the receptor in the signal transduction pathway.

Sequence 24 BP; 7 A; 3 C; 8 G; 6 T; 0 other;

Query Match	58.2%	Score 12.8;	DB 21;	Length 24;
Best Local Similarity	87.5%	Pred. No. 4.7e+03;		
Matches 14;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;

QY	1	CTGAGACCGATATCGG	16
Db	9	CAGAGACTGATATCGG	24

XX 31-AUG-1999; 99WO-US20047.
XX DNA sequences which comprises forming a population of heteroduplexes,
XX 04-SEP-1998; 98US-0099147.
XX isolating and amplifying mismatched heteroduplexes to form amplicons,
XX and determining the sequence of the amplicon. The methods are useful for
XX identifying polymorphic DNA sequences and for comparing a reference DNA
XX population with test populations for identifying sequences that are
XX different (e.g. mutated sequences). The method allows large scale
XX identification of polymorphic or mutated sequences in an individual.
XX AA289641-Z89646 represent the primers used in the method of the
XX invention.
SQ Sequence 34 BP; 8 A; 9 C; 9 G; 8 T; 0 other;
Query Match 58.2%; Score 12.8; DB 21; Length 34;
Best Local Similarity 87.5%; Pred. No. 4.9e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 AGACCGATATCGGCTT 19
DB 27 AGAGCGATATCGGCTT 12
RESULT 29
AA289642
ID AA289642 standard; DNA; 34 BP.
XX
XX AA289642;
XX
XX 28-JUN-2000 (first entry)
XX
XX Plasmid pUC19 primer 2.
XX
XX
XX Primer; pUC19; screening; polymorphism; mutation; ss.
XX
XX Synthetic.
XX
XX WO200014282-A1.
XX
XX 16-MAR-2000.
XX
XX 31-AUG-1999; 99WO-US20047.
XX
XX 04-SEP-1998; 98US-0099147.
XX
XX (LYNX-) LYNX THERAPEUTICS INC.
XX
XX PI Brenner S;
XX
XX WPI; 2000-257018/22.
XX
XX
XX Identifying polymorphic DNA sequences comprising forming heteroduplexes
XX PT and isolating and amplifying mismatched heteroduplexes to form
XX amplicons -
XX
XX Disclosure; Page 24; 27pp; English.

CC This invention describes a novel method (I) for identifying polymorphic
CC DNA sequences which comprises forming a population of heteroduplexes,
CC isolating and amplifying mismatched heteroduplexes to form amplicons,
CC and determining the sequence of the amplicon. The methods are useful for
CC identifying polymorphic DNA sequences and for comparing a reference DNA
CC population with test populations for identifying sequences that are
CC different (e.g. mutated sequences). The method allows large scale
CC identification of polymorphic or mutated sequences in an individual.
CC AA289641-Z89646 represent the primers used in the method of the
CC invention.
SQ Sequence 34 BP; 8 A; 9 C; 9 G; 8 T; 0 other;
Query Match 58.2%; Score 12.8; DB 21; Length 34;
Best Local Similarity 87.5%; Pred. No. 4.9e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 AGACCGATATCGGCTT 19
DB 12 AGAGCGATATCGGCTT 27
RESULT 30
AA289642/c
ID AA289642 standard; DNA; 34 BP.
XX
XX AA289642;
XX
XX 28-JUN-2000 (first entry)
XX
XX Plasmid pUC19 primer 2.
XX
XX
XX Primer; pUC19; screening; polymorphism; mutation; ss.
XX
XX Synthetic.
XX
XX WO200014282-A1.
XX
XX 16-MAR-2000.
XX
XX 31-AUG-1999; 99WO-US20047.
XX
XX 04-SEP-1998; 98US-0099147.
XX
XX (LYNX-) LYNX THERAPEUTICS INC.
XX
XX PI Brenner S;
XX
XX WPI; 2000-257018/22.
XX
XX
XX Identifying polymorphic DNA sequences comprising forming heteroduplexes
XX PT and isolating and amplifying mismatched heteroduplexes to form
XX amplicons -
XX
XX Disclosure; Page 24; 27pp; English.
XX
XX
XX This invention describes a novel method (I) for identifying polymorphic
XX DNA sequences which comprises forming a population of heteroduplexes,
XX isolating and amplifying mismatched heteroduplexes to form amplicons,
XX and determining the sequence of the amplicon. The methods are useful for
XX identifying polymorphic DNA sequences and for comparing a reference DNA
XX population with test populations for identifying sequences that are
XX different (e.g. mutated sequences). The method allows large scale
XX identification of polymorphic or mutated sequences in an individual.
XX AA289641-Z89646 represent the primers used in the method of the
XX invention.
SQ Sequence 34 BP; 8 A; 9 C; 9 G; 8 T; 0 other;
Query Match 58.2%; Score 12.8; DB 21; Length 34;
Best Local Similarity 87.5%; Pred. No. 4.9e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CC identification of polymorphic or mutated sequences in an individual.
CC AAZ89641-Z89646 represent the primers used in the method of the
CC invention.
XX
SQ Sequence 43 BP; 11 A; 10 C; 10 G; 12 T; 0 other;
Query Match 58.2%; Score 12.8; DB 21; Length 43;
Best Local Similarity 87.5%; Pred. No. 5e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 AGACCGATATCGCTCT 19
DB 18 AGACCGATATCGCTCT 33
RESULT 34
AAZ89643/c
ID AAZ89643 standard; DNA; 43 BP.
XX
AC AAZ89643;
XX
DT 28-JUN-2000 (first entry)
XX
DE Plasmid pUC19 primer 3.
XX
KM Primer; pUC19; screening; polymorphism; mutation; ss.
XX
OS Synthetic.
XX
PN WO200014282-A1.
XX
PD 16-MAR-2000.
XX
PF 31-AUG-1999; 99WO-US20047.
XX
PR 04-SEP-1998; 98US-0099147.
XX
PA (LYNX-) LYNX THERAPEUTICS INC.
XX
PI Brenner S;
XX
DR WPI; 2000-257018/22.
XX
PT Identifying polymorphic DNA sequences comprising forming heteroduplexes
PT and isolating and amplifying mismatched heteroduplexes to form
PT amplicons -
PS Disclosure; Page 25; 27pp; English.
XX
XX This invention describes a novel method (I) for identifying polymorphic
CC DNA sequences which comprises forming a population of heteroduplexes,
CC isolating and amplifying mismatched heteroduplexes to form amplicons,
CC and determining the sequence of the amplicon. The methods are useful for
CC identifying polymorphic DNA sequences and for comparing a reference DNA
CC population with test populations for identifying sequences that are
CC different (e.g. mutated sequences). The method allows large scale
CC identification of polymorphic or mutated sequences in an individual.
CC AAZ89641-Z89646 represent the primers used in the method of the
CC invention.
XX
SQ Sequence 43 BP; 11 A; 10 C; 10 G; 12 T; 0 other;
Query Match 58.2%; Score 12.8; DB 21; Length 43;
Best Local Similarity 87.5%; Pred. No. 5e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 AGACCGATATCGCTCT 19
DB 33 AGACCGATATCGCTCT 18
RESULT 35
AAZ89644

ID AAZ89644 standard; DNA; 43 BP.
XX
AC AAZ89644;
XX
DT 28-JUN-2000 (first entry)
XX
DE Plasmid pUC19 primer 4.
XX
KM Primer; pUC19; screening; polymorphism; mutation; ss.
XX
OS Synthetic.
XX
PN WO200014282-A1.
XX
PD 16-MAR-2000.
XX
PF 31-AUG-1999; 99WO-US20047.
XX
PR 04-SEP-1998; 98US-0099147.
XX
PA (LYNX-) LYNX THERAPEUTICS INC.
XX
PI Brenner S;
XX
DR WPI; 2000-257018/22.
XX
PT Identifying polymorphic DNA sequences comprising forming heteroduplexes
PT and isolating and amplifying mismatched heteroduplexes to form
PT amplicons -
PS Disclosure; Page 25; 27pp; English.
XX
XX This invention describes a novel method (I) for identifying polymorphic
CC DNA sequences which comprises forming a population of heteroduplexes,
CC isolating and amplifying mismatched heteroduplexes to form amplicons,
CC and determining the sequence of the amplicon. The methods are useful for
CC identifying polymorphic DNA sequences and for comparing a reference DNA
CC population with test populations for identifying sequences that are
CC different (e.g. mutated sequences). The method allows large scale
CC identification of polymorphic or mutated sequences in an individual.
CC AAZ89641-Z89646 represent the primers used in the method of the
CC invention.
XX
SQ Sequence 43 BP; 11 A; 11 C; 11 G; 10 T; 0 other;
Query Match 58.2%; Score 12.8; DB 21; Length 43;
Best Local Similarity 87.5%; Pred. No. 5e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 AGACCGATATCGCTCT 19
DB 15 AGACCGATATCGCTCT 30
RESULT 36
AAZ89644/c
ID AAZ89644 standard; DNA; 43 BP.
XX
AC AAZ89644;
XX
DT 28-JUN-2000 (first entry)
XX
DE Plasmid pUC19 primer 4.
XX
KM Primer; pUC19; screening; polymorphism; mutation; ss.
XX
OS Synthetic.
XX
PN WO200014282-A1.
XX
PD 16-MAR-2000.
XX
PF 31-AUG-1999; 99WO-US20047.

```
XX 04-SEP-1998; 98US-0099147.
PR (LYNX-) LYNX THERAPEUTICS INC.
PA
XX Brenner S;
XX WPI; 2000-257018/22.
DR
XX Identifying polymorphic DNA sequences comprising forming heteroduplexes
PT and isolating and amplifying mismatched heteroduplexes to form
PT amplicons -
XX
PS Disclosure; Page 25; 27pp; English.
XX
CC This invention describes a novel method (I) for identifying polymorphic
CC DNA sequences which comprises forming a population of heteroduplexes,
CC isolating and amplifying mismatched heteroduplexes to form amplicons,
CC and determining the sequence of the amplicon. The methods are useful for
CC identifying polymorphic DNA sequences and for comparing a reference DNA
CC population with test populations for identifying sequences that are
CC different (e.g. mutated sequences). The method allows large scale
CC identification of polymorphic or mutated sequences in an individual.
CC AA289641-289646 represent the primers used in the method of the
CC invention.
XX
SO Sequence 43 BP; 11 A; 11 C; 11 G; 10 T; 0 other;
XX
Query Match 58.2%; Score 12.8; DB 21; Length 43;
Best Local Similarity 87.5%; Pred. No. 5e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
OY 4 AGACCGATATCGGCT 19
DB 30 AGACCGATATCGGCT 15
XX
RESULT 37
ABI90430
ID ABI90430 standard; DNA; 24 BP.
XX
AC ABI90430;
XX
DT 15-FEB-2002 (first entry)
XX
DE Capture oligonucleotide zip ID#4017 oligo #1.
XX
XX Human; K-ras; PCR primer; probe; capture probe; mutation detection;
KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity;
KW cancer; oncogene; tumour suppressor; human papillomavirus; forensic;
KW environmental monitoring; food industry; feed industry; ss.
XX
OS Synthetic.
XX
XX WO200179548-A2.
XX
PD 25-OCT-2001.
XX
PF 04-APR-2001; 2001WO-US10958.
XX
PR 14-APR-2000; 2000US-197271P.
XX
XX (CORR ) CORNELL RES FOUND INC.
XX
XX Barany F, Zilvi M, Gerry NP, Favis R, Kliman R;
XX WPI; 2002-034366/04.
XX
XX Designing capture oligonucleotide probes for use on a support to which
PT complementary oligonucleotides hybridize with little mismatch -
XX
PS Example 5; Fig 25; 300pp; English.
```

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XX The present invention describes a method (M1) for designing capture
CC oligonucleotide probes (I) for use on a support to which complementary
CC oligonucleotide probes (II) will hybridize with little mismatch, where
CC (I) have melting temperatures within a narrow range. The method is useful
CC for detecting infectious diseases caused by bacterial infectious agents
CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
CC Epstein-Barr virus and polio virus, and parasitic infectious agents
CC selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
CC medinensis. The method is also useful for detecting genetic diseases such
CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
CC involved in DNA amplification, replication, recombination or repair, the
CC cancer is specifically associated with a gene selected from BRCA1 gene,
CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
CC method is also used for environmental monitoring, forensics and the food
CC and feed industry, detecting comprises scanning (using e.g. a scanning
CC electron microscope and infrared microscope) the support at the
CC particular sites and identifying if ligation of the oligonucleotide probe
CC has occurred and correlating (using a computer) identified ligation to a
CC presence or absence of the target nucleotide sequences. AB182074 to
CC AB197546 represent oligonucleotide sequences used in the exemplification
CC of the present invention.
XX
SO Sequence 24 BP; 4 A; 7 C; 8 G; 5 T; 0 other;
XX
Query Match 57.3%; Score 12.6; DB 24; Length 24;
Best Local Similarity 78.9%; Pred. No. 6e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
OY 1 CTGAGACCGATATCGGCT 19
DB 6 CTGAGACCGATATCGGCT 24
XX
RESULT 38
ABI90430/C
ID ABI90430 standard; DNA; 24 BP.
XX
AC ABI90430;
XX
DT 15-FEB-2002 (first entry)
XX
DE Capture oligonucleotide zip ID#4017 oligo #1.
XX
XX Human; K-ras; PCR primer; probe; capture probe; mutation detection;
KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity;
KW cancer; oncogene; tumour suppressor; human papillomavirus; forensic;
KW environmental monitoring; food industry; feed industry; ss.
XX
OS Synthetic.
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XX WO200179548-A2.
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PF 04-APR-2001; 2001WO-US10958.
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PR 14-APR-2000; 2000US-197271P.
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XX Barany F, Zilvi M, Gerry NP, Favis R, Kliman R;
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PS Example 5; Fig 25; 300pp; English.
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CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
CC Epstein-Barr virus and polio virus, and parasitic infectious agents,
CC selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
CC medinis. The method is also useful for detecting genetic diseases such
CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
CC involved in DNA amplification, replication, recombination or repair, the
CC cancer is specifically associated with a gene selected from BRCA1 gene,
CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
CC method is also used for environmental monitoring, forensics and the food
CC and feed industry, detecting comprises scanning (using e.g. a scanning
CC electron microscope and infrared microscope) the support at the
CC particular sites and identifying if ligation of the oligonucleotide probe
CC sets occurred and correlating (using a computer) identified ligation to a
CC presence or absence of the target nucleotide sequences. AB182074 to
CC AB197546 represent oligonucleotide sequences used in the exemplification
CC of the present invention.
XX

SO Sequence 24 BP; 4 A; 7 C; 8 G; 5 T; 0 other;

Query Match 57.3%; Score 12.6; DB 24; Length 24;
Best Local Similarity 78.9%; Pred. No. 6e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 AGACCGATATCGGTCCAG 22
DB 24 AGACCGATATCGGTCCAG 6

RESULT 39

AB190431
ID AB190431 standard; DNA; 24 BP.

AC AB190431;

DT 15-FEB-2002 (first entry)

DE Capture oligonucleotide zip ID#4017 oligo #2.

XX Human; K-ras; PCR primer; probe; capture probe; mutation detection;
KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
KM infection; 21 hydroxylase deficiency; Turner Syndrome; obesity;
KW cancer; oncogene; tumour suppressor; human papillomavirus; forensic;
KM environmental monitoring; food industry; feed industry; ss.

XX Synthetic.

XX WO200179548-A2.

XX PD 25-OCT-2001.

XX PF 04-APR-2001; 2001WO-US10958.

XX PR 14-APR-2000; 2000US-197271P.

XX PA (CORR) CORNELL RES FOUND INC.

XX PI Barany F, Zivvi M, Gerry NP, Favis R, Kliman R;

XX DR WPI; 2002-034366/04.

XX Designing capture oligonucleotide probes for use on a support to which
PT complementary oligonucleotides hybridize with little mismatch -
XX Example 5; Fig 25; 300pp; English.
PS

XX The present invention describes a method (M1) for designing capture
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CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
CC Epstein-Barr virus and polio virus, and parasitic infectious agents,
CC selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
CC medinis. The method is also useful for detecting genetic diseases such
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CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
CC involved in DNA amplification, replication, recombination or repair, the
CC cancer is specifically associated with a gene selected from BRCA1 gene,
CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
CC method is also used for environmental monitoring, forensics and the food
CC and feed industry, detecting comprises scanning (using e.g. a scanning
CC electron microscope and infrared microscope) the support at the
CC particular sites and identifying if ligation of the oligonucleotide probe
CC sets occurred and correlating (using a computer) identified ligation to a
CC presence or absence of the target nucleotide sequences. AB182074 to
CC AB197546 represent oligonucleotide sequences used in the exemplification
CC of the present invention.
XX

SO Sequence 24 BP; 5 A; 8 C; 7 G; 4 T; 0 other;

Query Match 57.3%; Score 12.6; DB 24; Length 24;
Best Local Similarity 78.9%; Pred. No. 6e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 AGACCGATATCGGTCCAG 22
DB 1 AGACCGATATCGGTCCAG 19

RESULT 40

AB190431/C
ID AB190431 standard; DNA; 24 BP.

AC AB190431;

DT 15-FEB-2002 (first entry)

DE Capture oligonucleotide zip ID#4017 oligo #2.

XX Human; K-ras; PCR primer; probe; capture probe; mutation detection;
KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
KM infection; 21 hydroxylase deficiency; Turner Syndrome; obesity;
KW cancer; oncogene; tumour suppressor; human papillomavirus; forensic;
KM environmental monitoring; food industry; feed industry; ss.

XX Synthetic.

XX WO200179548-A2.

XX PD 25-OCT-2001.

XX PF 04-APR-2001; 2001WO-US10958.

XX PR 14-APR-2000; 2000US-197271P.

XX PA (CORR) CORNELL RES FOUND INC.

XX PI Barany F, Zivvi M, Gerry NP, Favis R, Kliman R;

XX DR WPI; 2002-034366/04.

XX Designing capture oligonucleotide probes for use on a support to which
PT complementary oligonucleotides hybridize with little mismatch -
XX Example 5; Fig 25; 300pp; English.
PS

XX The present invention describes a method (M1) for designing capture
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CC oligonucleotide probes (II) will hybridise with little mismatch, where
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CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
CC Epstein-Barr virus and polio virus, and parasitic infectious agents
CC selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
CC medinensis. The method is also useful for detecting genetic diseases such
CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
CC involved in DNA amplification, replication, recombination or repair, the
CC cancer is specifically associated with a gene selected from BRCA1 gene,
CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
CC method is also used for environmental monitoring, forensics and the food
CC and feed industry, detecting comprises scanning (using e.g. a scanning
CC electron microscope and infrared microscope) the support at the
CC particular sites and identifying if ligation of the oligonucleotide probe
CC sets occurred and correlating (using a computer) identified ligation to a
CC presence or absence of the target nucleotide sequences. AB182074 to
CC AB197546 represent oligonucleotide sequences used in the exemplification
CC of the present invention.
XX
SQ Sequence 24 BP; 5 A; 8 C; 7 G; 4 T; 0 other;
Query Match 57.3%; Score 12.6; DB 24; Length 24;
Best Local Similarity 78.9%; Pred. No. 6e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 CTGAGACGATATCGGTCT 19
Db 19 CTGGGACCCATACGGGTCT 1

Search completed: June 14, 2003, 21:58:11
Job time : 218 secs

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OM nucleic - nucleic search, using sw model

Run on: June 14, 2003, 21:55:20 ; Search time 64 Seconds
(without alignments)
105,420 Million cell updates/sec

Title: US-09-532-001-1

Perfect score: 22
Sequence: 1 CTGAGACCGATATCGGCTCTCAG 22

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-Processing: Minimum Match 0%
Maximum Match 100%

Listing first 1000 summaries

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6: /cgn2_6/prodata/2/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13	59.1	44	4	US-09-042-353-391
2	13	59.1	44	4	US-09-042-353-391
3	13	59.1	44	4	US-08-758-417A-241
4	13	59.1	44	4	US-08-758-417A-241
5	12.4	56.4	30	1	US-08-235-503B-61
6	12.4	56.4	30	1	US-08-235-503B-61
7	12.4	56.4	30	5	PCT-US95-05265-61
8	12.4	56.4	30	5	PCT-US95-05265-61
9	12.4	56.4	32	2	US-08-956-047-22
10	12.4	56.4	32	2	US-08-956-047-22
11	12.2	55.5	33	1	US-08-447-422-1
12	12.2	55.5	33	1	US-08-447-422-1
13	12.2	55.5	33	3	US-09-213-053-8
14	12.2	55.5	33	3	US-09-213-053-8
15	12.2	55.5	33	3	US-09-213-053-9
16	12.2	55.5	33	3	US-09-213-053-9
17	12.2	55.5	33	3	US-09-213-053-28
18	12.2	55.5	33	3	US-09-213-053-28
19	12.2	55.5	33	3	US-09-213-053-29
20	12.2	55.5	33	3	US-09-213-053-29
21	12.2	55.5	28	1	US-08-235-503B-68
22	12.2	55.5	28	1	US-08-235-503B-68
23	12.2	54.5	28	1	US-08-235-503B-69
24	12.2	54.5	28	1	US-08-235-503B-69
25	12.2	54.5	28	5	PCT-US95-05265-68
26	12.2	54.5	28	5	PCT-US95-05265-68
27	12.2	54.5	28	5	PCT-US95-05265-69

C 28	12	54.5	28	5	PCT-US95-05265-69	Sequence 69, App1
C 29	12	54.5	37	1	US-08-402-964-3	Sequence 3, App1
C 30	12	54.5	37	1	US-08-402-964-3	Sequence 3, App1
C 31	12	54.5	47	4	US-09-641-638-720	Sequence 720, App
C 32	12	54.5	47	4	US-09-641-638-720	Sequence 720, App
C 33	11.8	53.6	34	3	US-09-213-053-21	Sequence 21, App1
C 34	11.8	53.6	34	3	US-09-213-053-21	Sequence 21, App1
C 35	11.8	53.6	45	1	US-07-967-693-43	Sequence 43, App1
C 36	11.8	53.6	45	1	US-07-967-693-43	Sequence 43, App1
C 37	11.8	53.6	45	1	US-08-195-072-41	Sequence 41, App1
C 38	11.8	53.6	45	1	US-08-195-072-41	Sequence 41, App1
C 39	11.8	53.6	45	1	US-08-195-735-41	Sequence 41, App1
C 40	11.8	53.6	45	1	US-08-195-735-41	Sequence 41, App1
C 41	11.8	53.6	45	1	US-08-195-747-41	Sequence 41, App1
C 42	11.8	53.6	45	1	US-08-195-747-41	Sequence 41, App1
C 43	11.8	53.6	45	1	US-08-446-884-41	Sequence 41, App1
C 44	11.8	53.6	45	1	US-08-446-884-41	Sequence 41, App1
C 45	11.8	53.6	45	1	US-08-195-073-41	Sequence 41, App1
C 46	11.8	53.6	45	1	US-08-195-073-41	Sequence 41, App1
C 47	11.8	53.6	45	1	US-08-198-175-41	Sequence 41, App1
C 48	11.8	53.6	45	1	US-08-198-175-41	Sequence 41, App1
C 49	11.8	53.6	45	2	US-08-443-153-41	Sequence 41, App1
C 50	11.8	53.6	45	2	US-08-443-153-41	Sequence 41, App1
C 51	11.8	53.6	45	3	US-08-442-807-41	Sequence 41, App1
C 52	11.8	53.6	45	3	US-08-442-807-41	Sequence 41, App1
C 53	11.6	52.7	48	1	US-08-049-503-10	Sequence 10, App1
C 54	11.6	52.7	48	1	US-08-049-503-10	Sequence 10, App1
C 55	11.4	51.8	18	2	US-08-124-981A-39	Sequence 39, App1
C 56	11.4	51.8	18	2	US-08-124-981A-39	Sequence 39, App1
C 57	11.4	51.8	18	3	US-09-037-190-44	Sequence 39, App1
C 58	11.4	51.8	18	3	US-09-037-190-44	Sequence 39, App1
C 59	11.4	51.8	18	3	US-09-037-190-44	Sequence 44, App1
C 60	11.4	51.8	18	3	US-09-037-192-44	Sequence 44, App1
C 61	11.4	51.8	18	3	US-09-037-192-44	Sequence 44, App1
C 62	11.4	51.8	18	3	US-09-037-143-44	Sequence 44, App1
C 63	11.4	51.8	18	4	US-09-049-691-79	Sequence 44, App1
C 64	11.4	51.8	18	4	US-09-049-691-79	Sequence 44, App1
C 65	11.4	51.8	18	4	US-09-049-691-79	Sequence 79, App1
C 66	11.4	51.8	18	4	US-09-332-346-44	Sequence 44, App1
C 67	11.4	51.8	18	4	US-09-332-346-44	Sequence 44, App1
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C 74	11.4	51.8	18	4	US-09-037-192-44	Sequence 44, App1
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C 76	11.4	51.8	39	4	US-08-944-368A-15	Sequence 15, App1
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C 78	11.4	51.8	39	4	US-09-820-764-15	Sequence 15, App1
C 79	11.4	51.8	41	3	US-08-783-853A-58	Sequence 58, App1
C 80	11.4	51.8	41	3	US-08-783-853A-58	Sequence 58, App1
C 81	11.4	51.8	41	3	US-08-783-853A-58	Sequence 58, App1
C 82	11.4	51.8	41	3	US-08-783-853A-58	Sequence 58, App1
C 83	11.4	51.8	41	3	US-09-344-050-58	Sequence 58, App1
C 84	11.4	51.8	41	4	US-09-344-050-58	Sequence 58, App1
C 85	11.4	51.8	41	4	US-09-344-050-58	Sequence 58, App1
C 86	11.4	51.8	41	4	US-09-344-050-58	Sequence 58, App1
C 87	11.4	51.8	47	4	US-09-167-375-7	Sequence 7, App1
C 88	11.4	51.8	47	4	US-09-167-375-7	Sequence 7, App1
C 89	11.4	51.8	48	1	US-07-834-539A-64	Sequence 64, App1
C 90	11.4	51.8	48	1	US-07-834-539A-64	Sequence 64, App1
C 91	11.4	51.8	48	1	US-08-053-131-112	Sequence 112, App
C 92	11.4	51.8	48	1	US-08-053-131-112	Sequence 112, App
C 93	11.4	51.8	48	1	US-08-645-641-112	Sequence 112, App
C 94	11.4	51.8	48	1	US-08-645-641-112	Sequence 112, App
C 95	11.4	51.8	48	1	US-07-853-408B-112	Sequence 112, App
C 96	11.4	51.8	48	1	US-07-853-408B-112	Sequence 112, App
C 97	11.4	51.8	48	1	US-08-096-762-112	Sequence 112, App
C 98	11.4	51.8	48	1	US-08-096-762-112	Sequence 112, App
C 99	11.4	51.8	48	2	US-08-800-353-64	Sequence 64, App1
C 100	11.4	51.8	48	2	US-08-800-353-64	Sequence 64, App1

C 101	11.4	51.8	48 2	US-08-308-865-112	Sequence 112, App	C 174	10.6	48.2	20 4	US-08-650-093C-49	Sequence 49, App1
C 102	11.4	51.8	48 2	US-08-308-865-112	Sequence 112, App	C 175	10.6	48.2	21 1	US-08-749-882A-3	Sequence 3, App1
C 103	11.4	51.8	48 4	US-09-042-353-305	Sequence 305, App	C 176	10.6	48.2	21 1	US-08-749-882A-3	Sequence 3, App1
C 104	11.4	51.8	48 4	US-09-042-353-305	Sequence 305, App	C 177	10.6	48.2	21 2	US-08-539-134-3	Sequence 3, App1
C 105	11.4	51.8	48 4	US-08-758-417A-153	Sequence 153, App	C 178	10.6	48.2	21 2	US-08-539-134-3	Sequence 3, App1
C 106	11.4	51.8	48 4	US-08-758-417A-153	Sequence 153, App	C 179	10.6	48.2	21 4	US-08-998-416-9	Sequence 9, App1
C 107	11.4	51.8	48 5	PCT-US92-06185-64	Sequence 64, App1	C 180	10.6	48.2	21 4	US-08-998-416-9	Sequence 9, App1
C 108	11.4	51.8	48 5	PCT-US92-06185-64	Sequence 64, App1	C 181	10.6	48.2	21 4	US-09-415-522-16	Sequence 16, App1
C 109	11.4	51.8	48 5	PCT-US92-10983-112	Sequence 112, App	C 182	10.6	48.2	21 4	US-09-415-522-16	Sequence 16, App1
C 110	11.4	51.8	48 5	PCT-US92-10983-112	Sequence 112, App	C 183	10.6	48.2	21 4	US-09-588-256-14	Sequence 14, App1
C 111	11.2	50.9	24 2	US-08-353-476-50	Sequence 50, App1	C 184	10.6	48.2	21 4	US-09-588-256-14	Sequence 14, App1
C 112	11.2	50.9	24 2	US-08-353-476-50	Sequence 50, App1	C 185	10.6	48.2	21 4	US-09-625-188-24	Sequence 24, App1
C 113	11.2	50.9	29 4	US-08-194-560-7	Sequence 7, App1	C 186	10.6	48.2	21 4	US-09-625-188-24	Sequence 24, App1
C 114	11.2	50.9	29 4	US-08-194-560-7	Sequence 7, App1	C 187	10.6	48.2	24 3	US-09-009-913-248	Sequence 248, App
C 115	11	50.0	20 3	US-09-058-489-70	Sequence 70, App1	C 188	10.6	48.2	24 3	US-09-009-913-248	Sequence 248, App
C 116	11	50.0	20 3	US-09-058-489-70	Sequence 70, App1	C 189	10.6	48.2	24 4	US-08-778-794A-136	Sequence 136, App
C 117	11	50.0	32 1	US-08-479-723A-77	Sequence 77, App1	C 190	10.6	48.2	24 4	US-08-778-794A-136	Sequence 136, App
C 118	11	50.0	32 1	US-08-479-723A-77	Sequence 77, App1	C 191	10.6	48.2	24 4	US-09-341-399-33	Sequence 33, App1
C 119	11	50.0	33 4	US-08-484-992A-5	Sequence 5, App1	C 192	10.6	48.2	24 4	US-09-341-399-33	Sequence 33, App1
C 120	11	50.0	33 4	US-08-484-992A-5	Sequence 5, App1	C 193	10.6	48.2	32 4	US-09-181-072-4	Sequence 4, App1
C 121	11	50.0	34 4	US-08-484-992A-3	Sequence 3, App1	C 194	10.6	48.2	32 4	US-09-181-072-4	Sequence 4, App1
C 122	11	50.0	36 1	US-08-402-964-2	Sequence 2, App1	C 195	10.6	48.2	33 1	US-08-038-071-5	Sequence 5, App1
C 123	11	50.0	36 1	US-08-402-964-2	Sequence 2, App1	C 196	10.6	48.2	33 1	US-08-038-071-5	Sequence 5, App1
C 124	11	50.0	36 1	US-08-402-964-2	Sequence 2, App1	C 197	10.6	48.2	34 4	US-09-302-620B-4	Sequence 4, App1
C 125	11	50.0	37 4	US-09-358-036-56	Sequence 56, App1	C 198	10.6	48.2	34 4	US-09-302-620B-4	Sequence 4, App1
C 126	11	50.0	37 4	US-09-358-036-56	Sequence 56, App1	C 199	10.6	48.2	36 4	US-09-540-014-30	Sequence 30, App1
C 127	11	50.0	46 1	US-08-271-880A-97	Sequence 97, App1	C 200	10.6	48.2	36 4	US-09-540-014-30	Sequence 30, App1
C 128	11	50.0	46 1	US-08-271-880A-97	Sequence 97, App1	C 201	10.6	48.2	38 1	US-08-147-710-5	Sequence 5, App1
C 129	11	50.0	46 1	US-08-271-880A-120	Sequence 120, App	C 202	10.6	48.2	38 1	US-08-147-710-5	Sequence 5, App1
C 130	11	50.0	46 1	US-08-271-880A-120	Sequence 120, App	C 203	10.6	48.2	38 1	US-08-458-090-5	Sequence 5, App1
C 131	11	50.0	46 2	US-08-910-408-97	Sequence 97, App1	C 204	10.6	48.2	38 1	US-08-458-090-5	Sequence 5, App1
C 132	11	50.0	46 2	US-08-910-408-97	Sequence 97, App1	C 205	10.6	48.2	38 2	US-08-457-887-5	Sequence 5, App1
C 133	11	50.0	46 2	US-08-910-408-120	Sequence 120, App	C 206	10.6	48.2	38 2	US-08-457-887-5	Sequence 5, App1
C 134	11	50.0	46 2	US-08-910-408-120	Sequence 120, App	C 207	10.6	48.2	39 1	US-08-147-000B-19	Sequence 19, App1
C 135	11	50.0	46 3	US-09-249-215-97	Sequence 97, App1	C 208	10.6	48.2	39 1	US-08-147-000B-19	Sequence 19, App1
C 136	11	50.0	46 3	US-09-249-215-97	Sequence 97, App1	C 209	10.6	48.2	39 3	US-08-863-813A-46	Sequence 46, App1
C 137	11	50.0	46 3	US-09-249-215-120	Sequence 120, App	C 210	10.6	48.2	41 4	US-09-143-077-1	Sequence 1, App1
C 138	11	50.0	46 3	US-09-249-215-120	Sequence 120, App	C 211	10.6	48.2	41 4	US-09-143-077-1	Sequence 1, App1
C 139	11	50.0	48 1	US-08-399-412A-104	Sequence 104, App	C 212	10.6	48.2	41 4	US-08-832-985-76	Sequence 76, App1
C 140	11	50.0	48 1	US-08-399-412A-104	Sequence 104, App	C 213	10.6	48.2	43 3	US-08-832-985-76	Sequence 76, App1
C 141	10.8	49.1	20 2	US-08-117-952-125	Sequence 75, App	C 214	10.6	48.2	43 3	US-08-832-985-76	Sequence 76, App1
C 142	10.8	49.1	20 2	US-08-117-952-125	Sequence 75, App	C 215	10.6	48.2	43 4	US-09-410-903-57	Sequence 57, App1
C 143	10.8	49.1	28 2	US-08-930-274-13	Sequence 13, App1	C 216	10.6	48.2	43 4	US-09-410-903-57	Sequence 57, App1
C 144	10.8	49.1	28 2	US-08-930-274-13	Sequence 13, App1	C 217	10.6	48.2	45 4	US-09-199-737-12	Sequence 12, App1
C 145	10.8	49.1	28 2	US-08-930-274-14	Sequence 14, App1	C 218	10.6	48.2	45 4	US-09-199-737-12	Sequence 12, App1
C 146	10.8	49.1	32 1	US-08-930-274-14	Sequence 14, App1	C 219	10.6	48.2	45 4	US-09-058-333A-12	Sequence 12, App1
C 147	10.8	49.1	32 1	US-08-442-063A-7	Sequence 7, App1	C 220	10.6	48.2	45 4	US-09-058-333A-12	Sequence 12, App1
C 148	10.8	49.1	34 2	US-08-442-063A-7	Sequence 7, App1	C 221	10.6	48.2	47 3	US-08-448-194-59	Sequence 59, App1
C 149	10.8	49.1	34 2	US-08-882-435-6	Sequence 6, App1	C 222	10.6	48.2	47 3	US-08-448-194-59	Sequence 59, App1
C 150	10.8	49.1	34 2	US-08-882-435-6	Sequence 6, App1	C 223	10.6	48.2	47 4	US-08-983-523-1	Sequence 1, App1
C 151	10.8	49.1	35 4	US-08-899-241-320	Sequence 220, App	C 224	10.6	48.2	47 4	US-08-983-523-1	Sequence 1, App1
C 152	10.8	49.1	35 4	US-08-899-241-320	Sequence 220, App	C 225	10.6	48.2	47 4	US-08-867-921-59	Sequence 59, App1
C 153	10.8	49.1	40 2	US-08-873-479-46	Sequence 46, App1	C 226	10.6	48.2	47 4	US-08-867-921-59	Sequence 59, App1
C 154	10.8	49.1	40 2	US-08-873-479-46	Sequence 46, App1	C 227	10.6	48.2	48 2	US-08-558-269-16	Sequence 16, App1
C 155	10.8	49.1	40 2	US-08-972-661A-32	Sequence 32, App1	C 228	10.6	48.2	48 2	US-08-558-269-16	Sequence 16, App1
C 156	10.8	49.1	40 2	US-08-972-661A-32	Sequence 32, App1	C 229	10.6	48.2	48 2	US-08-558-269-16	Sequence 16, App1
C 157	10.8	49.1	47 5	PCT-US93-09070-2	Sequence 2, App1	C 230	10.6	48.2	48 2	US-08-558-269-16	Sequence 16, App1
C 158	10.8	49.1	47 5	PCT-US93-09070-2	Sequence 2, App1	C 231	10.6	48.2	48 4	US-09-410-882-21	Sequence 21, App1
C 159	10.8	49.1	48 2	US-08-873-479-45	Sequence 45, App1	C 232	10.6	48.2	48 4	US-09-410-882-21	Sequence 21, App1
C 160	10.8	49.1	48 2	US-08-873-479-45	Sequence 45, App1	C 233	10.6	48.2	48 4	US-09-410-882-21	Sequence 21, App1
C 161	10.8	49.1	48 2	US-08-972-661A-31	Sequence 31, App1	C 234	10.6	48.2	49 4	US-08-983-523-2	Sequence 2, App1
C 162	10.8	49.1	48 2	US-08-972-661A-31	Sequence 31, App1	C 235	10.6	48.2	49 4	US-08-983-523-2	Sequence 2, App1
C 163	10.6	48.2	20 1	US-07-992-723A-24	Sequence 24, App1	C 236	10.6	48.2	50 2	US-08-566-398-29	Sequence 29, App1
C 164	10.6	48.2	20 1	US-07-992-723A-24	Sequence 24, App1	C 237	10.6	48.2	50 2	US-08-566-398-29	Sequence 29, App1
C 165	10.6	48.2	20 1	US-07-992-723A-24	Sequence 24, App1	C 238	10.6	48.2	50 2	US-08-566-398-29	Sequence 29, App1
C 166	10.6	48.2	20 1	US-07-992-723A-24	Sequence 24, App1	C 239	10.6	48.2	18 4	US-09-474-922A-89	Sequence 89, App1
C 167	10.6	48.2	20 2	US-07-952-277A-24	Sequence 24, App1	C 240	10.4	47.3	18 4	US-09-474-922A-89	Sequence 89, App1
C 168	10.6	48.2	20 2	US-07-952-277A-24	Sequence 24, App1	C 241	10.4	47.3	20 1	US-08-300-265-5	Sequence 5, App1
C 169	10.6	48.2	20 4	US-09-226-012-86	Sequence 86, App1	C 242	10.4	47.3	20 1	US-08-300-265-5	Sequence 5, App1
C 170	10.6	48.2	20 4	US-09-226-012-86	Sequence 86, App1	C 243	10.4	47.3	20 2	US-08-716-718-5	Sequence 5, App1
C 171	10.6	48.2	20 4	US-08-397-220B-49	Sequence 49, App1	C 244	10.4	47.3	20 2	US-08-716-718-5	Sequence 5, App1
C 172	10.6	48.2	20 4	US-08-397-220B-49	Sequence 49, App1	C 245	10.4	47.3	20 4	US-09-438-836A-5	Sequence 5, App1
C 173	10.6	48.2	20 4	US-08-650-093C-49	Sequence 49, App1	C 246	10.4	47.3	20 4	US-09-438-836A-5	Sequence 5, App1

247	10.4	47.3	21	1	US-08-306-254-4	Sequence 4, Appl1	C 320	10.4	47.3	36	2	US-08-418-085-24	Sequence 24, Appl1
C 248	10.4	47.3	21	1	US-08-306-254-4	Sequence 7, Appl1	C 321	10.4	47.3	36	4	US-09-099-011A-24	Sequence 24, Appl1
C 249	10.4	47.3	21	1	US-08-306-254-7	Sequence 7, Appl1	C 322	10.4	47.3	36	4	US-09-099-011A-24	Sequence 24, Appl1
C 250	10.4	47.3	21	1	US-08-306-254-7	Sequence 7, Appl1	C 323	10.4	47.3	37	1	US-08-402-964-4	Sequence 4, Appl1
C 252	10.4	47.3	22	4	US-08-467-044-2	Sequence 2, Appl1	C 324	10.4	47.3	37	1	US-08-402-964-4	Sequence 4, Appl1
C 253	10.4	47.3	22	4	US-09-291-541-22	Sequence 22, Appl1	C 325	10.4	47.3	39	3	US-08-481-739-3	Sequence 3, Appl1
C 254	10.4	47.3	22	4	US-09-291-541-22	Sequence 22, Appl1	C 326	10.4	47.3	39	3	US-08-481-739-3	Sequence 3, Appl1
C 255	10.4	47.3	24	1	US-08-433-783-30	Sequence 30, Appl1	C 327	10.4	47.3	39	3	US-09-428-589-3	Sequence 3, Appl1
C 256	10.4	47.3	24	1	US-08-433-783-30	Sequence 30, Appl1	C 328	10.4	47.3	39	4	US-09-428-589-3	Sequence 3, Appl1
C 257	10.4	47.3	24	2	US-08-337-358-30	Sequence 30, Appl1	C 329	10.4	47.3	40	1	US-08-021-667A-12	Sequence 12, Appl1
C 258	10.4	47.3	24	2	US-08-337-358-30	Sequence 30, Appl1	C 330	10.4	47.3	40	1	US-08-021-667A-12	Sequence 12, Appl1
C 259	10.4	47.3	24	5	PCT-US93-12144-30	Sequence 30, Appl1	C 331	10.4	47.3	40	1	US-08-410-544-12	Sequence 12, Appl1
C 260	10.4	47.3	24	5	PCT-US93-12144-30	Sequence 30, Appl1	C 332	10.4	47.3	40	1	US-08-410-544-12	Sequence 12, Appl1
C 261	10.4	47.3	24	5	PCT-US95-07537A-30	Sequence 30, Appl1	C 333	10.4	47.3	40	1	US-08-728-785A-12	Sequence 12, Appl1
C 262	10.4	47.3	24	5	PCT-US95-07537A-30	Sequence 30, Appl1	C 334	10.4	47.3	40	1	US-08-728-785A-12	Sequence 12, Appl1
C 263	10.4	47.3	24	5	PCT-US95-07537-30	Sequence 30, Appl1	C 335	10.4	47.3	43	1	US-08-473-096-8	Sequence 8, Appl1
C 264	10.4	47.3	24	5	PCT-US95-07537-30	Sequence 30, Appl1	C 336	10.4	47.3	43	1	US-08-473-096-8	Sequence 8, Appl1
C 265	10.4	47.3	26	2	US-08-859-998-892	Sequence 892, App	C 337	10.4	47.3	43	1	US-08-473-096-9	Sequence 9, Appl1
C 266	10.4	47.3	26	2	US-08-859-998-892	Sequence 892, App	C 338	10.4	47.3	43	1	US-08-473-096-9	Sequence 9, Appl1
C 267	10.4	47.3	26	4	US-09-225-928-892	Sequence 892, App	C 339	10.4	47.3	47	4	US-09-641-638-710	Sequence 710, App
C 268	10.4	47.3	26	4	US-09-225-928-892	Sequence 892, App	C 340	10.4	47.3	47	4	US-09-641-638-710	Sequence 710, App
C 269	10.4	47.3	29	1	US-08-408-133-3	Sequence 3, Appl1	C 341	10.4	47.3	47	4	US-09-641-638-1103	Sequence 1103, App
C 270	10.4	47.3	29	1	US-08-408-133-3	Sequence 3, Appl1	C 342	10.4	47.3	47	4	US-09-641-638-1103	Sequence 1103, App
C 271	10.4	47.3	29	1	US-08-454-683-3	Sequence 3, Appl1	C 343	10.4	47.3	48	1	US-08-741-881-4	Sequence 4, Appl1
C 272	10.4	47.3	29	1	US-08-454-683-3	Sequence 3, Appl1	C 344	10.4	47.3	48	1	US-08-741-881-4	Sequence 4, Appl1
C 273	10.4	47.3	29	2	US-08-116-778E-18	Sequence 18, Appl1	C 345	10.4	47.3	48	1	US-08-739-158-4	Sequence 4, Appl1
C 274	10.4	47.3	29	2	US-08-116-778E-18	Sequence 18, Appl1	C 346	10.4	47.3	48	1	US-08-739-158-4	Sequence 4, Appl1
C 275	10.4	47.3	29	2	US-08-454-680-3	Sequence 3, Appl1	C 347	10.4	47.3	48	2	US-08-739-167-4	Sequence 4, Appl1
C 276	10.4	47.3	29	2	US-08-454-680-3	Sequence 3, Appl1	C 348	10.4	47.3	48	2	US-08-739-167-4	Sequence 4, Appl1
C 277	10.4	47.3	29	2	US-08-438-562-18	Sequence 18, Appl1	C 349	10.4	47.3	48	3	US-08-404-796-4	Sequence 4, Appl1
C 278	10.4	47.3	29	2	US-08-438-562-18	Sequence 18, Appl1	C 350	10.4	47.3	48	3	US-08-404-796-4	Sequence 4, Appl1
C 279	10.4	47.3	29	2	US-08-483-528B-18	Sequence 18, Appl1	C 351	10.4	47.3	48	3	US-08-931-869-4	Sequence 4, Appl1
C 280	10.4	47.3	29	2	US-08-483-528B-18	Sequence 18, Appl1	C 352	10.4	47.3	48	3	US-08-931-869-4	Sequence 4, Appl1
C 281	10.4	47.3	29	3	US-08-673-799C-18	Sequence 18, Appl1	C 353	10.4	47.3	48	4	US-09-350-399-4	Sequence 4, Appl1
C 282	10.4	47.3	29	3	US-08-673-799C-18	Sequence 18, Appl1	C 354	10.4	47.3	48	4	US-09-350-399-4	Sequence 4, Appl1
C 283	10.4	47.3	29	4	US-09-393-385B-18	Sequence 18, Appl1	C 355	10.4	47.3	48	4	US-09-336-140A-4	Sequence 4, Appl1
C 284	10.4	47.3	29	4	US-09-393-385B-18	Sequence 18, Appl1	C 356	10.4	47.3	48	4	US-09-336-140A-4	Sequence 4, Appl1
C 285	10.4	47.3	29	4	US-09-325-328B-6	Sequence 6, Appl1	C 357	10.4	47.3	48	4	US-09-415-784-12	Sequence 12, Appl1
C 286	10.4	47.3	29	4	US-09-325-328B-6	Sequence 6, Appl1	C 358	10.4	47.3	48	4	US-09-415-784-12	Sequence 12, Appl1
C 287	10.4	47.3	31	1	US-08-482-882-31	Sequence 31, Appl1	C 359	10.4	47.3	48	4	US-09-415-785A-12	Sequence 12, Appl1
C 288	10.4	47.3	31	1	US-08-482-882-31	Sequence 31, Appl1	C 360	10.4	47.3	48	4	US-09-415-785A-12	Sequence 12, Appl1
C 289	10.4	47.3	31	1	US-08-483-389-31	Sequence 31, Appl1	C 361	10.4	47.3	48	4	US-08-944-465-12	Sequence 12, Appl1
C 290	10.4	47.3	31	1	US-08-483-389-31	Sequence 31, Appl1	C 362	10.4	47.3	48	4	US-08-944-465-12	Sequence 12, Appl1
C 291	10.4	47.3	31	2	US-08-487-113D-31	Sequence 31, Appl1	C 363	10.4	47.3	48	4	US-09-415-868-12	Sequence 12, Appl1
C 292	10.4	47.3	31	2	US-08-487-113D-31	Sequence 31, Appl1	C 364	10.4	47.3	48	4	US-09-415-868-12	Sequence 12, Appl1
C 293	10.4	47.3	31	2	US-08-473-503-31	Sequence 31, Appl1	C 365	10.4	47.3	48	4	US-09-415-900-12	Sequence 12, Appl1
C 294	10.4	47.3	31	2	US-08-473-503-31	Sequence 31, Appl1	C 366	10.4	47.3	48	4	US-09-415-900-12	Sequence 12, Appl1
C 295	10.4	47.3	31	2	US-08-318-157B-41	Sequence 41, Appl1	C 367	10.2	46.4	14	1	US-08-309-512-26	Sequence 26, Appl1
C 296	10.4	47.3	31	2	US-08-318-157B-41	Sequence 41, Appl1	C 368	10.2	46.4	14	1	US-08-309-512-26	Sequence 26, Appl1
C 297	10.4	47.3	31	2	US-08-483-932-31	Sequence 31, Appl1	C 369	10.2	46.4	20	2	US-08-500-635A-4	Sequence 4, Appl1
C 298	10.4	47.3	31	2	US-08-483-932-31	Sequence 31, Appl1	C 370	10.2	46.4	20	2	US-08-500-635A-4	Sequence 4, Appl1
C 299	10.4	47.3	31	2	US-08-678-194-1	Sequence 1, Appl1	C 371	10.2	46.4	20	4	US-09-312-183A-18	Sequence 18, Appl1
C 300	10.4	47.3	31	2	US-08-678-194-1	Sequence 1, Appl1	C 372	10.2	46.4	20	4	US-09-312-183A-18	Sequence 18, Appl1
C 301	10.4	47.3	31	2	US-08-720-420A-31	Sequence 31, Appl1	C 373	10.2	46.4	20	4	US-09-167-151-4	Sequence 4, Appl1
C 302	10.4	47.3	31	2	US-08-720-420A-31	Sequence 31, Appl1	C 374	10.2	46.4	20	4	US-09-167-151-4	Sequence 4, Appl1
C 303	10.4	47.3	31	3	US-08-714-017-31	Sequence 31, Appl1	C 375	10.2	46.4	20	4	US-09-360-416-56	Sequence 56, Appl1
C 304	10.4	47.3	31	3	US-08-714-017-31	Sequence 31, Appl1	C 376	10.2	46.4	20	4	US-09-360-416-56	Sequence 56, Appl1
C 305	10.4	47.3	31	3	US-08-475-680-31	Sequence 31, Appl1	C 377	10.2	46.4	23	4	US-09-103-478-11	Sequence 11, Appl1
C 306	10.4	47.3	31	3	US-08-475-680-31	Sequence 31, Appl1	C 378	10.2	46.4	23	4	US-09-103-478-11	Sequence 11, Appl1
C 307	10.4	47.3	31	4	US-08-890-011-1	Sequence 1, Appl1	C 379	10.2	46.4	23	4	US-09-193-931C-11	Sequence 11, Appl1
C 308	10.4	47.3	31	4	US-08-890-011-1	Sequence 1, Appl1	C 380	10.2	46.4	23	4	US-09-193-931C-11	Sequence 11, Appl1
C 309	10.4	47.3	31	4	US-09-171-945-2	Sequence 2, Appl1	C 381	10.2	46.4	24	3	US-09-157-177-51	Sequence 51, Appl1
C 310	10.4	47.3	31	4	US-09-171-945-2	Sequence 2, Appl1	C 382	10.2	46.4	24	3	US-09-157-177-51	Sequence 51, Appl1
C 311	10.4	47.3	31	4	US-09-262-724-1	Sequence 1, Appl1	C 383	10.2	46.4	24	3	US-09-157-177-84	Sequence 84, Appl1
C 312	10.4	47.3	31	4	US-09-262-724-1	Sequence 1, Appl1	C 384	10.2	46.4	24	3	US-09-157-177-84	Sequence 84, Appl1
C 313	10.4	47.3	33	1	US-08-170-290A-39	Sequence 39, Appl1	C 385	10.2	46.4	24	3	US-08-557-006C-10	Sequence 10, Appl1
C 314	10.4	47.3	33	1	US-08-170-290A-39	Sequence 39, Appl1	C 386	10.2	46.4	24	4	US-08-447-422-7	Sequence 7, Appl1
C 315	10.4	47.3	33	1	US-08-519-103-21	Sequence 21, Appl1	C 387	10.2	46.4	27	1	US-08-447-422-7	Sequence 7, Appl1
C 316	10.4	47.3	33	1	US-08-519-103-21	Sequence 21, Appl1	C 388	10.2	46.4	27	1	US-08-447-422-7	Sequence 7, Appl1
C 317	10.4	47.3	33	4	US-09-018-635-21	Sequence 21, Appl1	C 389	10.2	46.4	29	4	US-09-001-472-6	Sequence 6, Appl1
C 318	10.4	47.3	33	4	US-09-018-635-21	Sequence 21, Appl1	C 390	10.2	46.4	29	4	US-09-001-472-6	Sequence 6, Appl1
C 319	10.4	47.3	36	2	US-08-418-085-24	Sequence 24, Appl1	C 391	10.2	46.4	30	2	US-08-491-988-18	Sequence 18, Appl1
							C 392	10.2	46.4	30	2	US-08-491-988-18	Sequence 18, Appl1

393	10.2	46.4	30	3	US-09-078-670-10	Sequence 10, Appl	C 466	10.2	46.4	50	2	US-08-475-228A-586	Sequence 586, App
C 394	10.2	46.4	30	3	US-09-078-670-10	Sequence 10, Appl	C 467	10.2	46.4	50	3	US-08-482-080A-586	Sequence 586, App
C 395	10.2	46.4	30	3	US-09-182-859-29	Sequence 29, Appl	C 468	10.2	46.4	50	3	US-08-482-080A-586	Sequence 586, App
C 396	10.2	46.4	30	3	US-09-182-859-29	Sequence 29, Appl	C 469	10.2	46.4	50	4	US-09-354-947-586	Sequence 586, App
C 397	10.2	46.4	30	4	US-09-426-332-3	Sequence 3, Appl1	C 470	10.2	46.4	50	4	US-09-354-947-586	Sequence 586, App
C 398	10.2	46.4	30	4	US-09-426-332-3	Sequence 3, Appl1	C 471	10.2	46.4	50	5	PCT-US93-12388-586	Sequence 586, App
C 399	10.2	46.4	30	4	US-09-537-168-28	Sequence 28, Appl	C 472	10.2	46.4	50	5	PCT-US93-12388-586	Sequence 586, App
C 400	10.2	46.4	30	4	US-09-537-168-28	Sequence 28, Appl	C 473	10.2	46.4	18	4	US-09-058-947A-7	Sequence 7, Appl1
C 401	10.2	46.4	30	4	US-09-627-154-10	Sequence 10, Appl	C 474	10	45.5	18	4	US-08-974-102-19	Sequence 19, Appl1
C 402	10.2	46.4	30	4	US-09-627-154-10	Sequence 10, Appl	C 475	10	45.5	19	4	US-08-997-251-15	Sequence 15, Appl1
C 403	10.2	46.4	30	4	US-09-672-459-29	Sequence 29, Appl	C 476	10	45.5	19	4	US-08-997-251-15	Sequence 15, Appl1
C 404	10.2	46.4	30	4	US-09-672-459-29	Sequence 29, Appl	C 477	10	45.5	20	2	US-08-680-326-19	Sequence 19, Appl1
C 405	10.2	46.4	33	1	US-08-438-639-46	Sequence 46, Appl	C 478	10	45.5	20	2	US-08-680-326-19	Sequence 19, Appl1
C 406	10.2	46.4	33	1	US-08-438-639-46	Sequence 46, Appl	C 479	10	45.5	21	3	US-08-987-326-18	Sequence 18, Appl1
C 407	10.2	46.4	33	1	US-07-813-358A-46	Sequence 46, Appl	C 480	10	45.5	21	3	US-08-987-326-18	Sequence 18, Appl1
C 408	10.2	46.4	33	1	US-07-813-358A-46	Sequence 46, Appl	C 481	10	45.5	23	4	US-08-781-420-19	Sequence 19, Appl1
C 409	10.2	46.4	33	2	US-08-470-124-79	Sequence 79, Appl	C 482	10	45.5	23	4	US-08-781-420-19	Sequence 19, Appl1
C 410	10.2	46.4	33	2	US-08-470-124-79	Sequence 79, Appl	C 483	10	45.5	23	4	US-08-874-102-19	Sequence 19, Appl1
C 411	10.2	46.4	33	3	US-08-441-971-122	Sequence 122, Appl	C 484	10	45.5	23	4	US-08-874-102-19	Sequence 19, Appl1
C 412	10.2	46.4	33	3	US-08-441-971-122	Sequence 122, Appl	C 485	10	45.5	23	4	US-08-984-919A-19	Sequence 19, Appl1
C 413	10.2	46.4	33	4	US-08-221-653-122	Sequence 122, Appl	C 486	10	45.5	23	4	US-08-984-919A-19	Sequence 19, Appl1
C 414	10.2	46.4	33	4	US-08-221-653-122	Sequence 122, Appl	C 487	10	45.5	23	4	US-09-006-595A-19	Sequence 19, Appl1
C 415	10.2	46.4	33	4	US-08-442-144A-122	Sequence 122, Appl	C 488	10	45.5	23	4	US-09-006-595A-19	Sequence 19, Appl1
C 416	10.2	46.4	33	4	US-08-442-144A-122	Sequence 122, Appl	C 489	10	45.5	24	1	US-08-155-171B-22	Sequence 22, Appl1
C 417	10.2	46.4	33	4	US-08-441-970-122	Sequence 122, Appl	C 490	10	45.5	24	1	US-08-155-171B-22	Sequence 22, Appl1
C 418	10.2	46.4	33	4	US-08-441-970-122	Sequence 122, Appl	C 491	10	45.5	24	2	US-08-435-998A-22	Sequence 22, Appl1
C 419	10.2	46.4	34	3	US-08-787-091-12	Sequence 12, Appl	C 492	10	45.5	24	2	US-08-435-998A-22	Sequence 22, Appl1
C 420	10.2	46.4	34	3	US-08-787-091-12	Sequence 12, Appl	C 493	10	45.5	24	2	US-08-535-276-13	Sequence 13, Appl1
C 421	10.2	46.4	36	1	US-08-402-964-1	Sequence 1, Appl1	C 494	10	45.5	24	2	US-08-535-276-13	Sequence 13, Appl1
C 422	10.2	46.4	36	1	US-08-402-964-1	Sequence 1, Appl1	C 495	10	45.5	24	4	US-09-557-584A-26	Sequence 26, Appl1
C 423	10.2	46.4	36	1	US-08-291-932A-627	Sequence 627, Appl	C 496	10	45.5	24	4	US-09-557-584A-26	Sequence 26, Appl1
C 424	10.2	46.4	36	1	US-08-291-932A-627	Sequence 627, Appl	C 497	10	45.5	24	4	US-09-335-234-13	Sequence 13, Appl1
C 425	10.2	46.4	36	1	US-08-334-847-229	Sequence 229, Appl	C 498	10	45.5	25	1	US-08-155-171B-29	Sequence 29, Appl1
C 426	10.2	46.4	36	1	US-08-334-847-229	Sequence 229, Appl	C 499	10	45.5	25	1	US-08-155-171B-29	Sequence 29, Appl1
C 427	10.2	46.4	36	1	US-08-334-847-763	Sequence 763, Appl	C 500	10	45.5	25	1	US-08-155-171B-29	Sequence 29, Appl1
C 428	10.2	46.4	36	1	US-08-334-847-763	Sequence 763, Appl	C 501	10	45.5	25	1	US-08-378-588-18	Sequence 18, Appl1
C 429	10.2	46.4	36	1	US-08-363-240A-340	Sequence 340, Appl	C 502	10	45.5	25	1	US-08-378-588-18	Sequence 18, Appl1
C 430	10.2	46.4	36	1	US-08-363-240A-340	Sequence 340, Appl	C 503	10	45.5	25	2	US-08-811-094-18	Sequence 18, Appl1
C 431	10.2	46.4	36	1	US-08-363-240A-347	Sequence 347, Appl	C 504	10	45.5	25	2	US-08-811-094-18	Sequence 18, Appl1
C 432	10.2	46.4	36	1	US-08-363-240A-347	Sequence 347, Appl	C 505	10	45.5	25	2	US-08-435-998A-29	Sequence 29, Appl1
C 433	10.2	46.4	37	4	US-09-477-924-5	Sequence 5, Appl1	C 506	10	45.5	25	2	US-08-435-998A-29	Sequence 29, Appl1
C 434	10.2	46.4	37	4	US-09-477-924-5	Sequence 5, Appl1	C 507	10	45.5	25	4	US-09-102-831-7	Sequence 7, Appl1
C 435	10.2	46.4	38	1	US-08-373-124A-1324	Sequence 1324, Ap	C 508	10	45.5	25	4	US-09-102-831-7	Sequence 7, Appl1
C 436	10.2	46.4	38	1	US-08-373-124A-1324	Sequence 1324, Ap	C 509	10	45.5	25	4	US-09-102-831-7	Sequence 7, Appl1
C 437	10.2	46.4	38	1	US-08-435-628-1324	Sequence 1324, Ap	C 510	10	45.5	25	4	US-09-102-831-8	Sequence 8, Appl1
C 438	10.2	46.4	38	1	US-08-435-628-1324	Sequence 1324, Ap	C 511	10	45.5	25	4	US-09-102-831-9	Sequence 9, Appl1
C 439	10.2	46.4	38	3	US-09-182-859-28	Sequence 28, Appl	C 512	10	45.5	25	4	US-09-102-831-9	Sequence 9, Appl1
C 440	10.2	46.4	38	3	US-09-182-859-28	Sequence 28, Appl	C 513	10	45.5	25	4	US-09-102-831-10	Sequence 10, Appl1
C 441	10.2	46.4	38	4	US-09-537-168-27	Sequence 27, Appl	C 514	10	45.5	25	4	US-09-102-831-10	Sequence 10, Appl1
C 442	10.2	46.4	38	4	US-09-537-168-27	Sequence 27, Appl	C 515	10	45.5	25	5	PCT-US94-11121-18	Sequence 18, Appl1
C 443	10.2	46.4	38	4	US-09-672-459-28	Sequence 28, Appl	C 516	10	45.5	25	5	PCT-US94-11121-18	Sequence 18, Appl1
C 444	10.2	46.4	38	4	US-09-672-459-28	Sequence 28, Appl	C 517	10	45.5	26	2	US-08-770-565-15	Sequence 15, Appl1
C 445	10.2	46.4	38	4	US-09-375-318-7	Sequence 7, Appl1	C 518	10	45.5	26	2	US-08-770-565-15	Sequence 15, Appl1
C 446	10.2	46.4	38	4	US-09-375-318-7	Sequence 7, Appl1	C 519	10	45.5	26	2	US-08-770-565-15	Sequence 15, Appl1
C 447	10.2	46.4	39	3	US-08-845-546-22	Sequence 22, Appl	C 520	10	45.5	26	3	US-08-974-180-21	Sequence 21, Appl1
C 448	10.2	46.4	39	3	US-08-845-546-22	Sequence 22, Appl	C 521	10	45.5	26	3	US-08-974-180-21	Sequence 21, Appl1
C 449	10.2	46.4	39	6	5256648-22	Patent No. 5256648	C 522	10	45.5	27	1	US-08-363-585-19	Sequence 19, Appl1
C 450	10.2	46.4	39	6	5256648-22	Patent No. 5256648	C 523	10	45.5	27	1	US-08-363-585-19	Sequence 19, Appl1
C 451	10.2	46.4	40	4	US-09-171-025-17	Sequence 17, Appl	C 524	10	45.5	27	1	US-08-363-585-20	Sequence 20, Appl1
C 452	10.2	46.4	40	4	US-09-171-025-17	Sequence 17, Appl	C 525	10	45.5	27	1	US-08-363-585-22	Sequence 22, Appl1
C 453	10.2	46.4	43	1	US-08-720-899-24	Sequence 24, Appl	C 526	10	45.5	27	1	US-08-363-585-22	Sequence 22, Appl1
C 454	10.2	46.4	43	1	US-08-720-899-24	Sequence 24, Appl	C 527	10	45.5	27	4	US-08-584-040-3355	Sequence 3355, Ap
C 455	10.2	46.4	43	1	US-08-459-610-24	Sequence 24, Appl	C 528	10	45.5	27	4	US-08-584-040-3355	Sequence 3355, Ap
C 456	10.2	46.4	43	1	US-08-459-610-24	Sequence 24, Appl	C 529	10	45.5	27	4	US-08-584-040-3355	Sequence 3355, Ap
C 457	10.2	46.4	43	2	US-08-343-804-24	Sequence 24, Appl	C 530	10	45.5	27	4	US-08-584-040-6375	Sequence 6375, Ap
C 458	10.2	46.4	43	2	US-08-343-804-24	Sequence 24, Appl	C 531	10	45.5	27	4	US-08-584-040-6375	Sequence 6375, Ap
C 459	10.2	46.4	44	1	US-08-452-083-27	Sequence 27, Appl	C 532	10	45.5	27	4	US-08-679-645-1103	Sequence 1103, Ap
C 460	10.2	46.4	44	1	US-08-452-083-27	Sequence 27, Appl	C 533	10	45.5	28	3	US-08-974-180-6	Sequence 6, Appl1
C 461	10.2	46.4	50	1	US-08-171-389-586	Sequence 586, App	C 534	10	45.5	28	3	US-08-974-180-6	Sequence 6, Appl1
C 462	10.2	46.4	50	1	US-08-171-389-586	Sequence 586, App	C 535	10	45.5	29	3	US-08-824-692-18	Sequence 18, Appl1
C 463	10.2	46.4	50	1	US-08-123-936-586	Sequence 586, App	C 536	10	45.5	29	3	US-08-824-692-18	Sequence 18, Appl1
C 464	10.2	46.4	50	1	US-08-123-936-586	Sequence 586, App	C 537	10	45.5	29	4	US-09-183-412-36	Sequence 36, Appl1
C 465	10.2	46.4	50	2	US-08-475-228A-586	Sequence 586, App	C 538	10	45.5	29	4	US-09-183-412-36	Sequence 36, Appl1

539	10	45.5	30	4	US-09-230-405-15	Sequence 15, Appl	C 612	10	45.5	41	1	US-08-172-328-11	Sequence 11, Appl
C 540	10	45.5	30	4	US-09-230-405-15	Sequence 15, Appl	613	10	45.5	41	1	US-08-593-535-27	Sequence 27, Appl
C 541	10	45.5	31	4	US-08-679-645-359	Sequence 359, App	C 614	10	45.5	41	1	US-08-593-535-27	Sequence 27, Appl
C 542	10	45.5	31	4	US-08-679-645-359	Sequence 359, App	615	10	45.5	42	2	US-08-880-557-17	Sequence 17, Appl
C 543	10	45.5	31	4	US-09-383-143-50	Sequence 50, Appl	C 616	10	45.5	42	2	US-08-880-557-17	Sequence 17, Appl
C 544	10	45.5	31	4	US-09-383-143-50	Sequence 50, Appl	617	10	45.5	42	2	US-09-189-583-17	Sequence 17, Appl
C 545	10	45.5	32	2	US-08-002-324-6	Sequence 6, Appl1	C 618	10	45.5	42	3	US-09-189-583-17	Sequence 17, Appl
C 546	10	45.5	32	2	US-08-002-324-6	Sequence 6, Appl1	619	10	45.5	42	3	US-09-189-583-17	Sequence 17, Appl
C 547	10	45.5	32	5	PCT-US94-00261-6	Sequence 6, Appl1	C 620	10	45.5	42	4	US-09-402-631A-35	Sequence 35, Appl
C 548	10	45.5	32	5	PCT-US94-00261-6	Sequence 6, Appl1	621	10	45.5	42	4	US-08-592-406-5	Sequence 5, Appl1
C 549	10	45.5	33	1	US-08-212-372-7	Sequence 7, Appl1	C 622	10	45.5	44	1	US-08-592-406-5	Sequence 5, Appl1
C 550	10	45.5	33	1	US-08-212-372-7	Sequence 7, Appl1	623	10	45.5	45	4	US-09-363-970-26	Sequence 26, Appl
C 551	10	45.5	33	2	US-08-343-443B-73	Sequence 73, Appl	C 624	10	45.5	45	4	US-09-363-970-26	Sequence 26, Appl
C 552	10	45.5	33	2	US-08-343-443B-73	Sequence 73, Appl	625	10	45.5	47	1	US-08-340-820-26	Sequence 26, Appl
C 553	10	45.5	33	2	US-08-343-443B-73	Sequence 73, Appl	C 626	10	45.5	47	1	US-08-340-820-26	Sequence 26, Appl
C 554	10	45.5	33	2	US-08-343-443B-93	Sequence 93, Appl	627	10	45.5	47	1	US-08-172-328-10	Sequence 10, Appl
C 555	10	45.5	34	1	US-07-825-959-8	Sequence 8, Appl1	C 628	10	45.5	47	1	US-08-172-328-10	Sequence 10, Appl
C 556	10	45.5	34	1	US-07-825-959-8	Sequence 8, Appl1	629	10	45.5	47	1	US-08-172-328-10	Sequence 10, Appl
C 557	10	45.5	34	1	US-08-131-324-8	Sequence 8, Appl1	C 630	10	45.5	48	1	US-08-593-535-26	Sequence 26, Appl
C 558	10	45.5	34	1	US-08-131-324-8	Sequence 8, Appl1	631	10	45.5	48	1	US-08-593-535-26	Sequence 26, Appl
C 559	10	45.5	34	1	US-08-647-584-6	Sequence 6, Appl1	C 632	10	45.5	48	1	US-08-389-459A-14	Sequence 14, Appl
C 560	10	45.5	34	1	US-08-647-584-6	Sequence 6, Appl1	633	10	45.5	48	3	US-08-389-459A-14	Sequence 14, Appl
C 561	10	45.5	34	4	US-09-358-972-255	Sequence 255, App	C 634	10	45.5	48	3	US-08-987-867A-14	Sequence 14, Appl
C 562	10	45.5	34	4	US-09-358-972-255	Sequence 255, App	635	10	45.5	49	4	US-09-363-970-27	Sequence 27, Appl
C 563	10	45.5	34	4	US-09-406-064-48	Sequence 48, Appl	C 636	10	45.5	49	4	US-09-363-970-27	Sequence 27, Appl
C 564	10	45.5	34	4	US-09-406-064-48	Sequence 48, Appl	637	9.8	44.5	18	1	US-08-334-847-895	Sequence 895, App
C 565	10	45.5	34	4	US-09-383-316-95	Sequence 95, Appl	C 638	9.8	44.5	18	1	US-08-334-847-895	Sequence 895, App
C 566	10	45.5	34	4	US-09-383-316-95	Sequence 95, Appl	639	9.8	44.5	20	1	US-08-031-147A-14	Sequence 14, Appl
C 567	10	45.5	35	4	US-08-235-836C-25	Sequence 25, Appl	C 640	9.8	44.5	20	1	US-08-031-147A-14	Sequence 14, Appl
C 568	10	45.5	35	4	US-08-235-836C-25	Sequence 25, Appl	641	9.8	44.5	20	1	US-07-872-678A-20	Sequence 20, Appl
C 569	10	45.5	36	1	US-08-122-321A-3	Sequence 3, Appl1	C 642	9.8	44.5	20	1	US-07-872-678A-20	Sequence 20, Appl
C 570	10	45.5	36	1	US-08-122-321A-3	Sequence 3, Appl1	643	9.8	44.5	20	1	US-08-512-681-24	Sequence 24, Appl
C 571	10	45.5	36	1	US-07-941-523-16	Sequence 16, Appl	C 644	9.8	44.5	20	1	US-08-512-681-24	Sequence 24, Appl
C 572	10	45.5	36	1	US-07-941-523-16	Sequence 16, Appl	645	9.8	44.5	20	2	US-08-403-888A-10	Sequence 10, App
C 573	10	45.5	36	1	US-08-368-803-21	Sequence 21, Appl	C 646	9.8	44.5	20	2	US-08-403-888A-10	Sequence 10, App
C 574	10	45.5	36	1	US-08-368-803-21	Sequence 21, Appl	647	9.8	44.5	20	4	US-09-103-875-110	Sequence 110, App
C 575	10	45.5	36	2	US-08-578-096A-22	Sequence 22, Appl	C 648	9.8	44.5	20	4	US-09-103-875-110	Sequence 110, App
C 576	10	45.5	36	2	US-08-578-096A-22	Sequence 22, Appl	649	9.8	44.5	20	4	US-09-560-594-33	Sequence 33, Appl
C 577	10	45.5	36	3	US-08-881-772-3	Sequence 3, Appl1	C 650	9.8	44.5	20	4	US-09-560-594-33	Sequence 33, Appl
C 578	10	45.5	36	3	US-08-881-772-3	Sequence 3, Appl1	651	9.8	44.5	20	5	PCT-US94-02471-14	Sequence 14, Appl
C 579	10	45.5	36	3	US-08-790-517-12	Sequence 12, Appl	C 652	9.8	44.5	20	5	PCT-US94-02471-14	Sequence 14, Appl
C 580	10	45.5	36	3	US-08-790-517-12	Sequence 12, Appl	653	9.8	44.5	21	4	US-08-406-030A-2	Sequence 2, Appl1
C 581	10	45.5	36	3	US-09-240-426-22	Sequence 22, Appl	C 654	9.8	44.5	21	4	US-08-406-030A-2	Sequence 2, Appl1
C 582	10	45.5	36	3	US-09-240-426-22	Sequence 22, Appl	655	9.8	44.5	22	4	US-09-347-114A-54	Sequence 54, Appl
C 583	10	45.5	36	3	US-09-219-932-18	Sequence 18, Appl	C 656	9.8	44.5	22	4	US-09-347-114A-54	Sequence 54, Appl
C 584	10	45.5	36	3	US-09-219-932-18	Sequence 18, Appl	657	9.8	44.5	23	2	US-08-403-853-23	Sequence 23, Appl
C 585	10	45.5	36	4	US-09-362-831-22	Sequence 22, Appl	C 658	9.8	44.5	23	2	US-08-403-853-23	Sequence 23, Appl
C 586	10	45.5	36	4	US-09-362-831-22	Sequence 22, Appl	659	9.8	44.5	23	4	US-09-182-117-7	Sequence 7, Appl1
C 587	10	45.5	36	5	PCT-US94-10130-3	Sequence 3, Appl1	C 660	9.8	44.5	23	4	US-09-182-117-7	Sequence 7, Appl1
C 588	10	45.5	37	1	US-08-459-519-1	Sequence 1, Appl1	661	9.8	44.5	23	4	US-08-482-918-90	Sequence 90, Appl
C 589	10	45.5	37	1	US-08-459-519-1	Sequence 1, Appl1	662	9.8	44.5	23	4	US-08-482-918-90	Sequence 90, Appl
C 590	10	45.5	37	1	US-08-459-519-1	Sequence 1, Appl1	663	9.8	44.5	23	4	US-09-324-681-90	Sequence 90, Appl
C 591	10	45.5	37	4	US-09-358-036-55	Sequence 55, Appl	C 664	9.8	44.5	23	4	US-09-324-681-90	Sequence 90, Appl
C 592	10	45.5	37	4	US-09-358-036-55	Sequence 55, Appl	665	9.8	44.5	23	4	US-08-336-728A-90	Sequence 90, Appl
C 593	10	45.5	38	1	US-08-117-907-10	Sequence 10, Appl	C 666	9.8	44.5	23	4	US-08-336-728A-90	Sequence 90, Appl
C 594	10	45.5	38	1	US-08-117-907-10	Sequence 10, Appl	667	9.8	44.5	24	2	US-08-353-476-49	Sequence 49, Appl
C 595	10	45.5	38	3	US-08-453-040-10	Sequence 10, Appl	C 668	9.8	44.5	24	2	US-08-353-476-49	Sequence 49, Appl
C 596	10	45.5	38	3	US-08-453-040-10	Sequence 10, Appl	669	9.8	44.5	24	2	US-08-353-476-49	Sequence 49, Appl
C 597	10	45.5	38	6	5281520-25	Patent No. 5281520	C 670	9.8	44.5	24	4	US-09-347-114A-23	Sequence 23, Appl
C 598	10	45.5	38	6	5281520-25	Patent No. 5281520	671	9.8	44.5	24	4	US-09-347-114A-23	Sequence 23, Appl
C 599	10	45.5	39	1	US-08-197-770-16	Sequence 16, Appl	C 672	9.8	44.5	25	3	US-08-513-974B-13	Sequence 13, Appl
C 600	10	45.5	39	1	US-08-197-770-16	Sequence 16, Appl	673	9.8	44.5	25	3	US-08-513-974B-13	Sequence 13, Appl
C 601	10	45.5	39	4	US-08-973-124-303	Sequence 303, App	C 674	9.8	44.5	25	3	US-08-513-974B-13	Sequence 13, Appl
C 602	10	45.5	39	4	US-08-973-124-303	Sequence 303, App	675	9.8	44.5	26	2	US-08-859-998-860	Sequence 205, App
C 603	10	45.5	39	5	PCT-US96-08014-303	Sequence 303, App	C 676	9.8	44.5	26	2	US-08-859-998-860	Sequence 860, App
C 604	10	45.5	39	5	PCT-US96-08014-303	Sequence 303, App	677	9.8	44.5	26	2	US-08-859-998-860	Sequence 860, App
C 605	10	45.5	39	6	5223482-34	Patent No. 5223482	C 678	9.8	44.5	26	4	US-09-347-114A-39	Sequence 39, Appl
C 606	10	45.5	39	6	5223482-34	Patent No. 5223482	679	9.8	44.5	26	4	US-09-347-114A-39	Sequence 39, Appl
C 607	10	45.5	40	4	US-09-383-143-39	Sequence 39, Appl	C 680	9.8	44.5	26	4	US-09-325-928-860	Sequence 860, App
C 608	10	45.5	40	4	US-09-383-143-39	Sequence 39, Appl	681	9.8	44.5	26	4	US-09-325-928-860	Sequence 860, App
C 609	10	45.5	41	1	US-08-340-820-27	Sequence 27, Appl	C 682	9.8	44.5	27	5	PCT-US92-08094-34	Sequence 34, Appl
C 610	10	45.5	41	1	US-08-340-820-27	Sequence 27, Appl	683	9.8	44.5	27	2	US-08-951-718-2	Sequence 2, Appl1
C 611	10	45.5	41	1	US-08-172-328-11	Sequence 11, Appl	C 684	9.8	44.5	27	2	US-08-951-718-2	Sequence 2, Appl1

685	9.8	44.5	27	3	US-09-126-280-17	Sequence 17, Appl	758	9.8	44.5	36	3	US-09-213-053-12	Sequence 12, Appl
C 686	9.8	44.5	27	3	US-09-126-280-17	Sequence 17, Appl	759	9.8	44.5	36	3	US-09-213-053-13	Sequence 13, Appl
C 687	9.8	44.5	27	4	US-08-584-040-5232	Sequence 5232, Ap	C 760	9.8	44.5	36	3	US-09-213-053-16	Sequence 16, Appl
C 688	9.8	44.5	27	4	US-08-584-040-5232	Sequence 5232, Ap	C 761	9.8	44.5	36	3	US-09-213-053-16	Sequence 16, Appl
C 689	9.8	44.5	28	4	US-09-347-114A-45	Sequence 45, Appl	C 762	9.8	44.5	36	3	US-09-213-053-16	Sequence 16, Appl
C 690	9.8	44.5	28	4	US-09-347-114A-45	Sequence 45, Appl	C 763	9.8	44.5	36	3	US-09-213-053-17	Sequence 17, Appl
C 691	9.8	44.5	29	1	US-08-233-788A-27	Sequence 27, Appl	C 764	9.8	44.5	36	3	US-09-213-053-17	Sequence 17, Appl
C 692	9.8	44.5	29	1	US-08-233-788A-27	Sequence 27, Appl	C 765	9.8	44.5	37	2	US-08-874-678-14	Sequence 14, Appl
C 693	9.8	44.5	30	1	US-08-450-945-29	Sequence 29, Appl	C 766	9.8	44.5	37	2	US-08-874-678-14	Sequence 14, Appl
C 694	9.8	44.5	30	1	US-08-450-945-29	Sequence 29, Appl	C 767	9.8	44.5	37	3	US-08-643-839-14	Sequence 14, Appl
C 695	9.8	44.5	30	2	US-08-174-672D-73	Sequence 73, Appl	C 768	9.8	44.5	37	3	US-08-643-839-14	Sequence 14, Appl
C 696	9.8	44.5	30	2	US-08-174-672D-73	Sequence 73, Appl	C 769	9.8	44.5	37	4	US-09-348-886-14	Sequence 14, Appl
C 697	9.8	44.5	30	3	US-07-705-490-10	Sequence 10, Appl	C 770	9.8	44.5	37	4	US-09-348-886-14	Sequence 14, Appl
C 698	9.8	44.5	30	3	US-07-705-490-10	Sequence 10, Appl	C 771	9.8	44.5	38	3	US-08-724-752-8	Sequence 8, Appl
C 699	9.8	44.5	30	3	US-08-758-662-6	Sequence 6, Appl	C 772	9.8	44.5	38	3	US-08-724-752-8	Sequence 8, Appl
C 700	9.8	44.5	30	3	US-08-758-662-6	Sequence 6, Appl	C 773	9.8	44.5	38	3	US-09-213-053-20	Sequence 20, Appl
C 701	9.8	44.5	30	4	US-07-751-891B-10	Sequence 10, Appl	C 774	9.8	44.5	38	3	US-09-213-053-20	Sequence 20, Appl
C 702	9.8	44.5	30	4	US-07-751-891B-10	Sequence 10, Appl	C 775	9.8	44.5	39	4	US-09-262-773-101	Sequence 101, Appl
C 703	9.8	44.5	30	4	US-07-751-891B-10	Sequence 10, Appl	C 776	9.8	44.5	39	4	US-09-262-773-101	Sequence 101, Appl
C 704	9.8	44.5	30	4	US-07-751-891B-16	Sequence 16, Appl	C 777	9.8	44.5	40	1	US-08-032-846-35	Sequence 35, Appl
C 705	9.8	44.5	30	4	US-08-976-161-29	Sequence 29, Appl	C 778	9.8	44.5	40	1	US-08-032-846-35	Sequence 35, Appl
C 706	9.8	44.5	30	4	US-08-976-161-29	Sequence 29, Appl	C 779	9.8	44.5	40	1	US-08-474-636-35	Sequence 35, Appl
C 707	9.8	44.5	31	2	US-08-956-047-4	Sequence 4, Appl	C 780	9.8	44.5	40	4	US-08-474-636-35	Sequence 35, Appl
C 708	9.8	44.5	31	2	US-08-956-047-4	Sequence 4, Appl	C 781	9.8	44.5	41	1	US-08-530-492-79	Sequence 79, Appl
C 709	9.8	44.5	31	2	US-08-924-695A-9	Sequence 9, Appl	C 782	9.8	44.5	41	1	US-08-530-492-79	Sequence 79, Appl
C 710	9.8	44.5	31	2	US-08-924-695A-9	Sequence 9, Appl	C 783	9.8	44.5	41	4	US-08-906-517-79	Sequence 79, Appl
C 711	9.8	44.5	31	2	US-08-504-878A-3	Sequence 3, Appl	C 784	9.8	44.5	41	4	US-08-906-517-79	Sequence 79, Appl
C 712	9.8	44.5	31	3	US-08-504-878A-3	Sequence 3, Appl	C 785	9.8	44.5	41	4	US-09-293-569-5	Sequence 5, Appl
C 713	9.8	44.5	31	3	US-08-504-878A-3	Sequence 3, Appl	C 786	9.8	44.5	41	4	US-09-293-569-5	Sequence 5, Appl
C 714	9.8	44.5	31	4	US-09-246-277A-9	Sequence 9, Appl	C 787	9.8	44.5	41	4	US-09-363-970-13	Sequence 13, Appl
C 715	9.8	44.5	32	1	US-08-181-556-4	Sequence 4, Appl	C 788	9.8	44.5	42	1	US-09-363-970-13	Sequence 13, Appl
C 716	9.8	44.5	32	1	US-08-181-556-4	Sequence 4, Appl	C 789	9.8	44.5	42	1	US-08-530-492-145	Sequence 145, Appl
C 717	9.8	44.5	32	2	US-08-697-631A-1	Sequence 1, Appl	C 790	9.8	44.5	42	1	US-08-530-492-145	Sequence 145, Appl
C 718	9.8	44.5	32	2	US-08-697-631A-1	Sequence 1, Appl	C 791	9.8	44.5	42	1	US-08-466-033-156	Sequence 156, Appl
C 719	9.8	44.5	33	1	US-08-276-852-163	Sequence 163, App	C 792	9.8	44.5	42	1	US-08-466-033-156	Sequence 156, Appl
C 720	9.8	44.5	33	1	US-08-276-852-163	Sequence 163, App	C 793	9.8	44.5	42	1	US-08-444-733-156	Sequence 156, Appl
C 721	9.8	44.5	33	1	US-08-276-852-166	Sequence 166, App	C 794	9.8	44.5	42	1	US-08-444-733-156	Sequence 156, Appl
C 722	9.8	44.5	33	1	US-08-276-852-166	Sequence 166, App	C 795	9.8	44.5	42	2	US-08-464-134-156	Sequence 156, App
C 723	9.8	44.5	33	1	US-08-899-575-163	Sequence 163, App	C 796	9.8	44.5	42	2	US-08-464-134-156	Sequence 156, App
C 724	9.8	44.5	33	1	US-08-899-575-163	Sequence 163, App	C 797	9.8	44.5	42	2	US-08-461-361-156	Sequence 156, App
C 725	9.8	44.5	33	1	US-08-899-575-166	Sequence 166, App	C 798	9.8	44.5	42	2	US-08-461-361-156	Sequence 156, App
C 726	9.8	44.5	33	1	US-08-899-575-166	Sequence 166, App	C 799	9.8	44.5	42	2	US-08-485-910-156	Sequence 156, App
C 727	9.8	44.5	33	1	US-08-899-575-163	Sequence 163, App	C 800	9.8	44.5	42	2	US-08-485-910-156	Sequence 156, App
C 728	9.8	44.5	33	1	US-08-899-575-163	Sequence 163, App	C 801	9.8	44.5	42	4	US-08-906-517-145	Sequence 145, App
C 729	9.8	44.5	33	1	US-08-899-575-166	Sequence 166, App	C 802	9.8	44.5	42	4	US-08-906-517-145	Sequence 145, App
C 730	9.8	44.5	33	1	US-08-899-575-166	Sequence 166, App	C 803	9.8	44.5	45	1	US-08-554-133-2	Sequence 2, Appl
C 731	9.8	44.5	33	3	US-08-819-177-29	Sequence 29, Appl	C 804	9.8	44.5	45	1	US-08-554-133-2	Sequence 2, Appl
C 732	9.8	44.5	33	3	US-08-819-177-29	Sequence 29, Appl	C 805	9.8	44.5	49	4	US-09-538-709-122	Sequence 122, App
C 733	9.8	44.5	33	4	US-08-943-136-14	Sequence 14, Appl	C 806	9.8	44.5	49	4	US-09-538-709-122	Sequence 122, App
C 734	9.8	44.5	33	4	US-08-943-136-14	Sequence 14, Appl	C 807	9.8	44.5	49	4	US-09-538-709-1285	Sequence 1285, Ap
C 735	9.8	44.5	33	4	US-08-973-518-14	Sequence 14, Appl	C 808	9.8	44.5	49	4	US-09-538-709-1285	Sequence 1285, Ap
C 736	9.8	44.5	33	4	US-08-973-518-14	Sequence 14, Appl	C 809	9.8	44.5	50	1	US-07-977-696C-55	Sequence 55, Appl
C 737	9.8	44.5	33	5	PCT-US95-08743-163	Sequence 163, App	C 810	9.8	44.5	50	1	US-07-977-696C-55	Sequence 55, Appl
C 738	9.8	44.5	33	5	PCT-US95-08743-163	Sequence 163, App	C 811	9.8	44.5	50	1	US-08-129-930B-55	Sequence 55, Appl
C 739	9.8	44.5	33	5	PCT-US95-08743-166	Sequence 166, App	C 812	9.8	44.5	50	1	US-08-129-930B-55	Sequence 55, Appl
C 740	9.8	44.5	33	5	PCT-US95-08743-166	Sequence 166, App	C 813	9.8	44.5	50	4	US-08-976-288A-55	Sequence 55, Appl
C 741	9.8	44.5	35	1	US-08-451-240-39	Sequence 39, Appl	C 814	9.8	44.5	50	4	US-08-976-288A-55	Sequence 55, Appl
C 742	9.8	44.5	35	1	US-08-451-240-39	Sequence 39, Appl	C 815	9.8	43.6	19	4	US-09-305-927-33	Sequence 33, Appl
C 743	9.8	44.5	35	1	US-08-664-449-20	Sequence 20, Appl	C 816	9.8	43.6	19	4	US-09-305-927-33	Sequence 33, Appl
C 744	9.8	44.5	35	1	US-08-664-449-20	Sequence 20, Appl	C 817	9.8	43.6	20	1	US-08-460-130-1	Sequence 1, Appl
C 745	9.8	44.5	35	2	US-08-470-846A-35	Sequence 35, Appl	C 818	9.8	43.6	20	1	US-08-460-130-1	Sequence 1, Appl
C 746	9.8	44.5	35	2	US-08-470-846A-35	Sequence 35, Appl	C 819	9.8	43.6	20	1	US-08-484-607A-56	Sequence 56, Appl
C 747	9.8	44.5	35	3	US-08-967-272-5	Sequence 5, Appl	C 820	9.8	43.6	20	1	US-08-484-607A-56	Sequence 56, Appl
C 748	9.8	44.5	35	3	US-08-967-272-5	Sequence 5, Appl	C 821	9.8	43.6	20	1	US-08-557-139-30	Sequence 30, Appl
C 749	9.8	44.5	35	5	PCT-US94-12591-39	Sequence 39, Appl	C 822	9.8	43.6	20	1	US-08-557-139-30	Sequence 30, Appl
C 750	9.8	44.5	35	5	PCT-US94-12591-39	Sequence 39, Appl	C 823	9.8	43.6	20	3	US-08-962-169-56	Sequence 56, Appl
C 751	9.8	44.5	36	1	US-08-291-932A-445	Sequence 445, App	C 824	9.8	43.6	20	3	US-08-962-169-56	Sequence 56, Appl
C 752	9.8	44.5	36	1	US-08-291-932A-445	Sequence 445, App	C 825	9.8	43.6	20	4	US-09-487-368A-129	Sequence 129, App
C 753	9.8	44.5	36	1	US-08-363-240A-914	Sequence 914, App	C 826	9.8	43.6	22	6	5202236-29	Patent No. 5202236
C 754	9.8	44.5	36	1	US-08-363-240A-914	Sequence 914, App	C 827	9.8	43.6	22	6	5202236-29	Patent No. 5202236
C 755	9.8	44.5	36	1	US-08-311-486C-855	Sequence 855, App	C 828	9.8	43.6	23	2	US-08-859-998-816	Sequence 816, App
C 756	9.8	44.5	36	1	US-08-311-486C-855	Sequence 855, App	C 829	9.8	43.6	23	2	US-08-859-998-816	Sequence 816, App
C 757	9.8	44.5	36	3	US-09-213-053-12	Sequence 12, Appl	C 830	9.8	43.6	23	2	US-09-213-053-12	Sequence 12, Appl

831	9.6	43.6	23	4	US-09-225-928-816	Sequence 816, App	C 904	9.6	43.6	36	4	US-08-848-760B-18	Sequence 18, Appl
C 832	9.6	43.6	23	4	US-09-225-928-816	Sequence 816, App	C 905	9.6	43.6	36	4	US-09-374-962-17	Sequence 17, Appl
C 833	9.6	43.6	23	4	US-09-122-126B-10	Sequence 10, Appl	C 906	9.6	43.6	36	4	US-09-374-962-17	Sequence 17, Appl
C 834	9.6	43.6	23	4	US-09-122-126B-10	Sequence 10, Appl	C 907	9.6	43.6	38	1	US-08-390-850-857	Sequence 857, App
C 835	9.6	43.6	24	1	US-08-460-344-38	Sequence 38, Appl	C 908	9.6	43.6	38	1	US-08-390-850-857	Sequence 857, App
C 836	9.6	43.6	24	1	US-08-460-344-38	Sequence 38, Appl	C 909	9.6	43.6	38	1	US-08-390-850-923	Sequence 923, App
C 837	9.6	43.6	24	1	US-08-460-344-62	Sequence 62, Appl	C 910	9.6	43.6	38	1	US-08-390-850-923	Sequence 923, App
C 838	9.6	43.6	24	1	US-08-460-344-62	Sequence 62, Appl	C 911	9.6	43.6	38	1	US-08-390-850-931	Sequence 931, App
C 839	9.6	43.6	24	1	US-08-133-598A-38	Sequence 38, Appl	C 912	9.6	43.6	38	1	US-08-390-850-931	Sequence 931, App
C 840	9.6	43.6	24	1	US-08-133-598A-38	Sequence 38, Appl	C 913	9.6	43.6	38	1	US-08-373-124A-259	Sequence 259, App
C 841	9.6	43.6	24	1	US-08-133-598A-62	Sequence 62, Appl	C 914	9.6	43.6	38	1	US-08-373-124A-259	Sequence 259, App
C 842	9.6	43.6	24	1	US-08-133-598A-62	Sequence 62, Appl	C 915	9.6	43.6	38	1	US-08-373-124A-1346	Sequence 1346, Ap
C 843	9.6	43.6	24	1	US-08-558-420-3	Sequence 3, Appl	C 916	9.6	43.6	38	1	US-08-373-124A-1346	Sequence 1346, Ap
C 844	9.6	43.6	24	1	US-08-558-420-3	Sequence 3, Appl	C 917	9.6	43.6	38	1	US-08-373-124A-1750	Sequence 1750, Ap
C 845	9.6	43.6	24	1	US-08-886-999-38	Sequence 38, Appl	C 918	9.6	43.6	38	1	US-08-373-124A-1750	Sequence 1750, Ap
C 846	9.6	43.6	24	1	US-08-886-999-38	Sequence 38, Appl	C 919	9.6	43.6	38	1	US-08-373-124A-1936	Sequence 1936, Ap
C 847	9.6	43.6	24	1	US-08-886-999-62	Sequence 62, Appl	C 920	9.6	43.6	38	1	US-08-373-124A-1936	Sequence 1936, Ap
C 848	9.6	43.6	24	1	US-08-886-999-62	Sequence 62, Appl	C 921	9.6	43.6	38	1	US-08-373-124A-2292	Sequence 2292, Ap
C 849	9.6	43.6	24	2	US-08-353-476-51	Sequence 51, Appl	C 922	9.6	43.6	38	1	US-08-373-124A-2292	Sequence 2292, Ap
C 850	9.6	43.6	24	2	US-08-353-476-51	Sequence 51, Appl	C 923	9.6	43.6	38	1	US-08-373-124A-2428	Sequence 2428, Ap
C 851	9.6	43.6	24	5	PCT-US93-05085-39	Sequence 39, Appl	C 924	9.6	43.6	38	1	US-08-373-124A-2428	Sequence 2428, Ap
C 852	9.6	43.6	24	5	PCT-US93-05085-39	Sequence 39, Appl	C 925	9.6	43.6	38	1	US-08-373-124A-2476	Sequence 2476, Ap
C 853	9.6	43.6	25	2	US-08-590-674-1	Sequence 1, Appl	C 926	9.6	43.6	38	1	US-08-373-124A-2476	Sequence 2476, Ap
C 854	9.6	43.6	25	2	US-08-590-674-1	Sequence 1, Appl	C 927	9.6	43.6	38	1	US-08-435-634-857	Sequence 857, App
C 855	9.6	43.6	25	2	US-08-590-674-1	Sequence 1, Appl	C 928	9.6	43.6	38	1	US-08-435-634-857	Sequence 857, App
C 856	9.6	43.6	25	4	US-09-315-793-19	Sequence 19, Appl	C 929	9.6	43.6	38	1	US-08-435-634-923	Sequence 923, App
C 857	9.6	43.6	25	4	US-09-315-793-19	Sequence 19, Appl	C 930	9.6	43.6	38	1	US-08-435-634-923	Sequence 923, App
C 858	9.6	43.6	25	4	US-09-395-345-34	Sequence 34, Appl	C 931	9.6	43.6	38	1	US-08-435-634-931	Sequence 931, App
C 859	9.6	43.6	26	1	US-08-664-449-21	Sequence 21, Appl	C 932	9.6	43.6	38	1	US-08-435-634-931	Sequence 931, App
C 860	9.6	43.6	26	1	US-08-664-449-21	Sequence 21, Appl	C 933	9.6	43.6	38	1	US-08-435-628-259	Sequence 259, App
C 861	9.6	43.6	28	3	US-08-474-700B-6	Sequence 6, Appl	C 934	9.6	43.6	38	1	US-08-435-628-259	Sequence 259, App
C 862	9.6	43.6	28	3	US-08-474-700B-6	Sequence 6, Appl	C 935	9.6	43.6	38	1	US-08-435-628-1346	Sequence 1346, Ap
C 863	9.6	43.6	28	4	US-09-338-420-6	Sequence 6, Appl	C 936	9.6	43.6	38	1	US-08-435-628-1346	Sequence 1346, Ap
C 864	9.6	43.6	28	4	US-09-338-420-6	Sequence 6, Appl	C 937	9.6	43.6	38	1	US-08-435-628-1750	Sequence 1750, Ap
C 865	9.6	43.6	28	5	PCT-US95-05812-6	Sequence 6, Appl	C 938	9.6	43.6	38	1	US-08-435-628-1750	Sequence 1750, Ap
C 866	9.6	43.6	28	5	PCT-US95-05812-6	Sequence 6, Appl	C 939	9.6	43.6	38	1	US-08-435-628-1936	Sequence 1936, Ap
C 867	9.6	43.6	29	4	US-08-843-572E-7	Sequence 7, Appl	C 940	9.6	43.6	38	1	US-08-435-628-1936	Sequence 1936, Ap
C 868	9.6	43.6	29	4	US-08-843-572E-7	Sequence 7, Appl	C 941	9.6	43.6	38	1	US-08-435-628-2292	Sequence 2292, Ap
C 869	9.6	43.6	30	2	US-08-353-372A-31	Sequence 31, Appl	C 942	9.6	43.6	38	1	US-08-435-628-2292	Sequence 2292, Ap
C 870	9.6	43.6	30	2	US-08-353-372A-31	Sequence 31, Appl	C 943	9.6	43.6	38	1	US-08-435-628-2428	Sequence 2428, Ap
C 871	9.6	43.6	30	3	US-08-462-436-4	Sequence 4, Appl	C 944	9.6	43.6	38	1	US-08-435-628-2428	Sequence 2428, Ap
C 872	9.6	43.6	30	3	US-08-462-436-4	Sequence 4, Appl	C 945	9.6	43.6	38	1	US-08-435-628-2476	Sequence 2476, Ap
C 873	9.6	43.6	30	3	US-08-465-275-4	Sequence 4, Appl	C 946	9.6	43.6	38	1	US-08-435-628-2476	Sequence 2476, Ap
C 874	9.6	43.6	30	3	US-08-465-275-4	Sequence 4, Appl	C 947	9.6	43.6	38	2	US-08-292-620A-2162	Sequence 2162, Ap
C 875	9.6	43.6	30	4	US-09-493-352A-6	Sequence 6, Appl	C 948	9.6	43.6	38	2	US-08-292-620A-2162	Sequence 2162, Ap
C 876	9.6	43.6	30	4	US-09-493-352A-6	Sequence 6, Appl	C 949	9.6	43.6	38	3	US-09-071-845-2162	Sequence 2162, Ap
C 877	9.6	43.6	30	4	US-08-057-430A-22	Sequence 22, Appl	C 950	9.6	43.6	38	3	US-09-071-845-2162	Sequence 2162, Ap
C 878	9.6	43.6	30	4	US-08-057-430A-22	Sequence 22, Appl	C 951	9.6	43.6	39	1	US-08-527-734-19	Sequence 19, Appl
C 879	9.6	43.6	30	4	US-08-640-877-4	Sequence 4, Appl	C 952	9.6	43.6	39	1	US-08-527-734-19	Sequence 19, Appl
C 880	9.6	43.6	30	4	US-08-640-877-4	Sequence 4, Appl	C 953	9.6	43.6	39	1	US-08-527-734-20	Sequence 20, Appl
C 881	9.6	43.6	31	4	US-08-679-645-497	Sequence 497, App	C 954	9.6	43.6	39	1	US-08-527-734-20	Sequence 20, Appl
C 882	9.6	43.6	31	4	US-08-679-645-497	Sequence 497, App	C 955	9.6	43.6	39	4	US-08-592-459-9	Sequence 9, Appl
C 883	9.6	43.6	33	1	US-08-664-449-22	Sequence 22, Appl	C 956	9.6	43.6	39	4	US-08-592-459-9	Sequence 9, Appl
C 884	9.6	43.6	33	1	US-08-664-449-22	Sequence 22, Appl	C 957	9.6	43.6	39	5	PCT-US91-08525-9	Sequence 9, Appl
C 885	9.6	43.6	33	4	US-09-257-580-6	Sequence 6, Appl	C 958	9.6	43.6	39	5	PCT-US91-08525-9	Sequence 9, Appl
C 886	9.6	43.6	33	4	US-09-257-580-6	Sequence 6, Appl	C 959	9.6	43.6	39	5	PCT-US93-04384-33	Sequence 33, Appl
C 887	9.6	43.6	34	3	US-08-951-923-54	Sequence 54, Appl	C 960	9.6	43.6	39	5	PCT-US93-04384-33	Sequence 33, Appl
C 888	9.6	43.6	34	3	US-08-951-923-54	Sequence 54, Appl	C 961	9.6	43.6	40	4	US-09-485-737B-9	Sequence 9, Appl
C 889	9.6	43.6	34	3	US-08-961-083-452	Sequence 452, App	C 962	9.6	43.6	40	4	US-09-485-737B-9	Sequence 9, Appl
C 890	9.6	43.6	34	3	US-08-961-083-452	Sequence 452, App	C 963	9.6	43.6	42	1	US-08-401-908-25	Sequence 25, Appl
C 891	9.6	43.6	35	2	US-08-458-970A-4	Sequence 4, Appl	C 964	9.6	43.6	42	1	US-08-401-908-25	Sequence 25, Appl
C 892	9.6	43.6	35	2	US-08-458-970A-4	Sequence 4, Appl	C 965	9.6	43.6	44	1	US-07-991-587A-4	Sequence 4, Appl
C 893	9.6	43.6	35	4	US-09-374-962-18	Sequence 18, Appl	C 966	9.6	43.6	44	1	US-07-991-587A-4	Sequence 4, Appl
C 894	9.6	43.6	35	4	US-09-374-962-18	Sequence 18, Appl	C 967	9.6	43.6	44	1	US-08-309-985-4	Sequence 4, Appl
C 895	9.6	43.6	36	1	US-08-644-664B-2	Sequence 2, Appl	C 968	9.6	43.6	44	1	US-08-309-985-4	Sequence 4, Appl
C 896	9.6	43.6	36	1	US-08-644-664B-2	Sequence 2, Appl	C 969	9.6	43.6	44	1	US-08-105-483-41	Sequence 41, Appl
C 897	9.6	43.6	36	2	US-08-761-277A-2	Sequence 2, Appl	C 970	9.6	43.6	44	1	US-08-105-483-41	Sequence 41, Appl
C 898	9.6	43.6	36	2	US-08-761-277A-2	Sequence 2, Appl	C 971	9.6	43.6	44	1	US-08-073-962-41	Sequence 41, Appl
C 899	9.6	43.6	36	4	US-08-821-278A-5	Sequence 5, Appl	C 972	9.6	43.6	44	1	US-08-073-962-41	Sequence 41, Appl
C 900	9.6	43.6	36	4	US-08-821-278A-5	Sequence 5, Appl	C 973	9.6	43.6	44	1	US-07-714-687-53	Sequence 53, Appl
C 901	9.6	43.6	36	4	US-08-821-278A-9	Sequence 9, Appl	C 974	9.6	43.6	44	1	US-07-714-687-53	Sequence 53, Appl
C 902	9.6	43.6	36	4	US-08-821-278A-9	Sequence 9, Appl	C 975	9.6	43.6	44	1	US-08-224-391-92	Sequence 92, Appl
C 903	9.6	43.6	36	4	US-08-848-760B-18	Sequence 18, Appl	C 976	9.6	43.6	44	1	US-08-224-391-92	Sequence 92, Appl

977 9.6 43.6 44 1 US-08-484-304-92 Sequence 92, Appl
c 978 9.6 43.6 44 1 US-08-484-304-92 Sequence 92, Appl
979 9.6 43.6 44 1 US-08-487-412-41 Sequence 41, Appl
c 980 9.6 43.6 44 1 US-08-487-412-41 Sequence 41, Appl
981 9.6 43.6 44 1 US-08-709-209-41 Sequence 41, Appl
c 982 9.6 43.6 44 1 US-08-709-209-41 Sequence 41, Appl
983 9.6 43.6 44 1 US-08-458-101-41 Sequence 41, Appl
c 984 9.6 43.6 44 1 US-08-458-101-41 Sequence 41, Appl
985 9.4 42.7 17 2 US-08-970-269A-14 Sequence 14, Appl
c 986 9.4 42.7 17 2 US-08-970-269A-14 Sequence 14, Appl
987 9.4 42.7 17 4 US-09-407-562-14 Sequence 14, Appl
c 988 9.4 42.7 17 4 US-09-407-562-14 Sequence 14, Appl
989 9.4 42.7 17 4 US-09-375-318-49 Sequence 49, Appl
c 990 9.4 42.7 17 4 US-09-375-318-49 Sequence 49, Appl
991 9.4 42.7 18 4 US-09-122-400B-19 Sequence 19, Appl
c 992 9.4 42.7 18 4 US-09-122-400B-19 Sequence 19, Appl
993 9.4 42.7 20 1 US-08-356-405-11 Sequence 11, Appl
c 994 9.4 42.7 20 1 US-08-356-405-11 Sequence 11, Appl
995 9.4 42.7 20 2 US-08-910-629A-58 Sequence 58, Appl
c 996 9.4 42.7 20 2 US-08-910-629A-58 Sequence 58, Appl
997 9.4 42.7 20 2 US-09-289-368-52 Sequence 52, Appl
c 998 9.4 42.7 20 2 US-09-289-368-52 Sequence 52, Appl
999 9.4 42.7 20 3 US-08-888-998-7 Sequence 7, Appl
c1000 9.4 42.7 20 3 US-08-888-998-7 Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-09-042-353-391
Sequence 391, Application US/09042353
Patent No. 6255458
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 421
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042.353
FILING DATE: 13-MAR-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-JUL-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US96/16433
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/758,417
FILING DATE: 02-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/21803
FILING DATE: 01-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 014643--009040US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 391:
SEQUENCE CHARACTERISTICS:
LENGTH: 44 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-042-353-391
Query Match 59.1%; Score 13; DB 4; Length 44;
Best Local Similarity 76.2%; Ptd. No. 3.9e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2 TGAGCCGATATCGTCTCG 22
DB 9 TGAGAGTGAATCTGTCCAG 29
RESULT 2
US-09-042-353-391/c
Sequence 391, Application US/09042353
Patent No. 6255458
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 421
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,353
FILING DATE: 13-MAR-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US96/16433
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/758,417
FILING DATE: 02-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/21803
FILING DATE: 01-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 014643-009040US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 391:
SEQUENCE CHARACTERISTICS:
LENGTH: 44 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-042-353-391

Query Match 59.1%; Score 13; DB 4; Length 44;

Best Local Similarity 76.2%; Pred. No. 3.9e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 CTGAGACCATATCGCTCTCA 21
Db 29 CTGGACAGATTTCACCTCA 9

RESULT 3
US-08-758-417A-241
Sequence 241, Application US/08758417A
Patent No. 6300129
GENERAL INFORMATION:
APPLICANT: Lomborg, Nils
Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for
Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 417
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/758,417A
FILING DATE: 02-DEC-1996
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-JUL-1993
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Serafini, Andrew T.
REGISTRATION NUMBER: 41,303
REFERENCE/DOCKET NUMBER: 014643-009030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 241:
SEQUENCE CHARACTERISTICS:
LENGTH: 44 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 241:
US-08-758-417A-241

Query Match 59.1%; Score 13; DB 4; Length 44;

Best Local Similarity 76.2%; Pred. No. 3.9e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 TGAGACCGATATCGTCTCAG 22
Db 9 TGAGAGTGAATCTGTCCAG 29

RESULT 4

US-08-758-417A-241/C

Sequence 241, Application US/08758417A

Patent No. 6300129

GENERAL INFORMATION:

APPLICANT: Lomborg, Nile

KAY, Robert M.

TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for

Producing Heterologous Antibodies

NUMBER OF SEQUENCES: 417

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/758,417A

FILING DATE: 02-Dec-1996

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/728,463

FILING DATE: 10-OCT-1996

APPLICATION NUMBER: US 08/544,404

FILING DATE: 10-OCT-1995

APPLICATION NUMBER: US 08/352,322

FILING DATE: 07-DEC-1994

APPLICATION NUMBER: US 08/209,741

FILING DATE: 09-MAR-1994

APPLICATION NUMBER: US 08/165,699

FILING DATE: 10-DEC-1993

APPLICATION NUMBER: US 08/161,739

FILING DATE: 03-DEC-1993

APPLICATION NUMBER: US 08/155,301

FILING DATE: 18-NOV-1993

APPLICATION NUMBER: US 08/096,762

FILING DATE: 22-JUL-1993

APPLICATION NUMBER: US 08/053,131

FILING DATE: 26-APR-1993

APPLICATION NUMBER: US 07/990,860

FILING DATE: 16-DEC-1992

ATTORNEY/AGENT INFORMATION:

NAME: Serafini, Andrew T.

REGISTRATION NUMBER: 41,303

REFERENCE/DOCKET NUMBER: 014643-009030US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 241:

SEQUENCE CHARACTERISTICS:

LENGTH: 44 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

SEQUENCE DESCRIPTION: SEQ ID NO: 241:

US-08-758-417A-241

Query Match

59.1%; Score 13; DB 4; Length 44;

Best Local Similarity 76.2%; Pred. No. 3.9e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CTGAGACCGATATCGTCTCA 21
Db 29 CTGAGACGATTTCACTCTCA 9

RESULT 5

US-08-235-503B-61

Sequence 61, Application US/08235503B

Patent No. 5563036

GENERAL INFORMATION:

APPLICANT: Peterson, Michael G

APPLICANT: Baichwal, Vijay R

APPLICANT: Strulovici, Berta

TITLE OF INVENTION: TRANSCRIPTION FACTOR-DNA ASSAY

NUMBER OF SEQUENCES: 75

CORRESPONDENCE ADDRESSES:

ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT

STREET: 4 Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-4187

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/235,503B

FILING DATE: 29-APR-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Osman, Richard A

REGISTRATION NUMBER: 36,627

REFERENCE/DOCKET NUMBER: A-59332/RAO

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 781-1989

TELEFAX: (415) 398-3249

TELEX: 910 277299

INFORMATION FOR SEQ ID NO: 61:

SEQUENCE CHARACTERISTICS:

LENGTH: 30 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-08-235-503B-61

Query Match 56.4%; Score 12.4; DB 1; Length 30;

Best Local Similarity 72.7%; Pred. No. 7.8e+02;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CTGAGACCGATATCGTCTCAG 22
Db 5 CTGTCACGAAACGGTACCAG 26

RESULT 6

US-08-235-503B-61/C

Sequence 61, Application US/08235503B

Patent No. 5563036

GENERAL INFORMATION:

APPLICANT: Peterson, Michael G

APPLICANT: Baichwal, Vijay R

APPLICANT: Strulovici, Berta

TITLE OF INVENTION: TRANSCRIPTION FACTOR-DNA ASSAY

NUMBER OF SEQUENCES: 75

CORRESPONDENCE ADDRESSES:

ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT

STREET: 4 Embarcadero Center, Suite 3400

CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/235,503B
FILING DATE: 29-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A
REGISTRATION NUMBER: 36,627
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 398-3249
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-235-503B-61

Query Match 56.4%; Score 12.4; DB 1; Length 30;
Best Local Similarity 72.7%; Pred. No. 7.8e+02;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CTGAGACCGATATCGCTCTAG 22
DB 26 CTGCTACCGTTTCGGTACCAG 5

RESULT 7
PCT-US95-05265-61
Sequence 61, Application PC/TUS9505265
GENERAL INFORMATION:
APPLICANT: TULARIK, INC.
TITLE OF INVENTION: TRANSCRIPTION FACTOR-DNA BINDING ASSAY
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05265
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/235,503
FILING DATE: 29-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: FP-59232-PC/RAO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299

INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
PCT-US95-05265-61

Query Match 56.4%; Score 12.4; DB 5; Length 30;
Best Local Similarity 72.7%; Pred. No. 7.8e+02;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CTGAGACCGATATCGCTCTAG 22
DB 5 CTGCTACCGAAACGGTACCAG 26

RESULT 8
PCT-US95-05265-61/c
Sequence 61, Application PC/TUS9505265
GENERAL INFORMATION:
APPLICANT: TULARIK, INC.
TITLE OF INVENTION: TRANSCRIPTION FACTOR-DNA BINDING ASSAY
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05265
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/235,503
FILING DATE: 29-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: FP-59232-PC/RAO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
PCT-US95-05265-61

Query Match 56.4%; Score 12.4; DB 5; Length 30;
Best Local Similarity 72.7%; Pred. No. 7.8e+02;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CTGAGACCGATATCGCTCTAG 22
DB 26 CTGCTACCGTTTCGGTACCAG 5

RESULT 9
US-08-956-047-22
Sequence 22, Application US/08956047

Patent No. 5882924
GENERAL INFORMATION:
APPLICANT: Fritz, Hans-Joachim
APPLICANT: Hennecke, Frank
APPLICANT: Kolmar, Harald
TITLE OF INVENTION: Genetic Selection, by Means of Signal
TITLE OF INVENTION: Transduction in Microorganisms, of Proteins which are
TITLE OF INVENTION: Capable of Ligand Binding
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Finnegan, Henderson, Parabow, Garrett & Dunner
STREET: 1300 I Street, N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,047
FILING DATE: 22-OCT-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/257,669
FILING DATE: 08-JUN-1994
APPLICATION NUMBER: DE P 43 19 296.3
FILING DATE: 10-JUN-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pohlman, Sandra M.
REGISTRATION NUMBER: P39,691
REFERENCE/DOCKET NUMBER: 05552.1368-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-956-047-22

Query Match 56.4%; Score 12.4; DB 2; Length 32;
Best Local Similarity 92.9%; Pred. No. 7.8e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CGATATCGCTCTCA 21
DB 9 CGATATCGCTCTCA 22

RESULT 10
US-08-956-047-22/C
Sequence 22, Application US/08956047
Patent No. 5882924
GENERAL INFORMATION:
APPLICANT: Fritz, Hans-Joachim
APPLICANT: Hennecke, Frank
APPLICANT: Kolmar, Harald
TITLE OF INVENTION: Genetic Selection, by Means of Signal
TITLE OF INVENTION: Transduction in Microorganisms, of Proteins which are
TITLE OF INVENTION: Capable of Ligand Binding
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Finnegan, Henderson, Parabow, Garrett & Dunner
STREET: 1300 I Street, N.W., Suite 600
CITY: Washington
STATE: D.C.

COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,047
FILING DATE: 22-OCT-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/257,669
FILING DATE: 08-JUN-1994
APPLICATION NUMBER: DE P 43 19 296.3
FILING DATE: 10-JUN-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pohlman, Sandra M.
REGISTRATION NUMBER: P39,691
REFERENCE/DOCKET NUMBER: 05552.1368-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-956-047-22

Query Match 56.4%; Score 12.4; DB 2; Length 32;
Best Local Similarity 92.9%; Pred. No. 7.8e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGAGACCATATCG 15
DB 22 TGAGACCATATCG 9

RESULT 11
US-08-447-422-1
Sequence 1, Application US/08447422
Patent No. 5686579
GENERAL INFORMATION:
APPLICANT: SHAMI, Ezekiel Y.
APPLICANT: ROTHSTEIN, Aser
APPLICANT: RAMJESINGH, Mohanb
TITLE OF INVENTION: Use of Antibody/Antigen Interactions To
TITLE OF INVENTION: Protect or Modulate Biological Activity
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,422
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/081,410
FILING DATE: 22-JUN-1993
APPLICATION NUMBER: US 07/938,505
FILING DATE: 31-AUG-1992

```
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/205,748
; FILING DATE: 21-JUN-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 17923/102 HYL1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 29
; OTHER INFORMATION: /mod_base= 1
;
US-08-447-422-1
;
Query Match      55.5%; Score 12.2; DB 1; Length 33;
Best Local Similarity 70.6%; Pred. No. 1e+03;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      5 GACCGATATCGCTCA 21
Db      5 GACCGAATGCTCTBA 21

RESULT 12
US-08-447-422-1/c
; Sequence 1, Application US/08447422
; Patent No. 5686579
; GENERAL INFORMATION:
; APPLICANT: SHAMI, Ezekiel Y.
; APPLICANT: ROTHSTEIN, Aser
; APPLICANT: RAMJESINGH, Mohabir
; TITLE OF INVENTION: Use of Antibody/Antigen Interactions To
; TITLE OF INVENTION: Protect or Modulate Biological Activity
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/447,422
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/081,410
; FILING DATE: 22-JUN-1993
; APPLICATION NUMBER: US 07/938,505
; FILING DATE: 31-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/205,748
; FILING DATE: 21-JUN-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 17923/102 HYL1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
```

```
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 29
; OTHER INFORMATION: /mod_base= 1
;
US-08-447-422-1
;
Query Match      55.5%; Score 12.2; DB 1; Length 33;
Best Local Similarity 70.6%; Pred. No. 1e+03;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      2 TGAGACCGATATCGCTC 18
Db      21 TVAGSACRATRTCGTC 5

RESULT 13
US-09-213-053-8
; Sequence 8, Application US/09213053
; Patent No. 6159477
; GENERAL INFORMATION:
; APPLICANT: AUDONNET, Jean-Christophe
; APPLICANT: BAUDU, Philippe
; TITLE OF INVENTION: CANINE HERPESVIRUS BASED RECOMBINANT LIVE VACCINE, IN
; TITLE OF INVENTION: PARTICULAR AGAINST CANINE DISTEMPER, RABIES OR THE
; FILE REFERENCE: 454313-2200
; CURRENT APPLICATION NUMBER: US/09/213,053
; CURRENT FILING DATE: 1998-12-16
; EARLIER APPLICATION NUMBER: 9608242
; EARLIER FILING DATE: 1996-06-27
; EARLIER APPLICATION NUMBER: PCT/FR97/01115
; EARLIER FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 8
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
;
US-09-213-053-8
;
Query Match      55.5%; Score 12.2; DB 3; Length 33;
Best Local Similarity 82.4%; Pred. No. 1e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      5 GACCGATATCGCTCA 21
Db      17 GATCGATATCGGCCCA 33

RESULT 14
US-09-213-053-8/c
; Sequence 8, Application US/09213053
; Patent No. 6159477
; GENERAL INFORMATION:
; APPLICANT: AUDONNET, Jean-Christophe
; APPLICANT: BAUDU, Philippe
; TITLE OF INVENTION: CANINE HERPESVIRUS BASED RECOMBINANT LIVE VACCINE, IN
; TITLE OF INVENTION: PARTICULAR AGAINST CANINE DISTEMPER, RABIES OR THE
; FILE REFERENCE: 454313-2200
; CURRENT APPLICATION NUMBER: US/09/213,053
; CURRENT FILING DATE: 1998-12-16
; EARLIER APPLICATION NUMBER: 9608242
```

```
; EARLIER FILING DATE: 1996-06-27
; EARLIER APPLICATION NUMBER: PCT/FR97/01115
; EARLIER FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide
US-09-213-053-8
```

```
Query Match      55.5%; Score 12.2; DB 3; Length 33;
Best Local Similarity 82.4%; Pred. No. 1e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 TGAGACCGATTCGATC 18
DB      33 TGGGCGCATTCATC 17
```

```
RESULT 15
US-09-213-053-9
; Sequence 9, Application US/09213053
; Patent No. 6159477
; GENERAL INFORMATION:
; APPLICANT: AUDONNET, Jean-Christophe
; APPLICANT: BAUDU, Philippe
; TITLE OF INVENTION: CANINE HERPESVIRUS BASED RECOMBINANT LIVE VACCINE, IN
; TITLE OF INVENTION: PARTICULAR AGAINST CANINE DISTEMPER, RABIES OR THE
; TITLE OF INVENTION: PARAINFLUENZA 2 VIRUS
; FILE REFERENCE: 454313-2200
; CURRENT APPLICATION NUMBER: US/09/213.053
; CURRENT FILING DATE: 1998-12-16
; EARLIER APPLICATION NUMBER: 9608242
; EARLIER FILING DATE: 1996-06-27
; EARLIER APPLICATION NUMBER: PCT/FR97/01115
; EARLIER FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide
US-09-213-053-9
```

```
Query Match      55.5%; Score 12.2; DB 3; Length 33;
Best Local Similarity 82.4%; Pred. No. 1e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 TGAGACCGATTCGATC 18
DB      5 TGGGCGCATTCATC 21
```

```
RESULT 16
US-09-213-053-9/c
; Sequence 9, Application US/09213053
; Patent No. 6159477
; GENERAL INFORMATION:
; APPLICANT: AUDONNET, Jean-Christophe
; APPLICANT: BAUDU, Philippe
; TITLE OF INVENTION: CANINE HERPESVIRUS BASED RECOMBINANT LIVE VACCINE, IN
; TITLE OF INVENTION: PARTICULAR AGAINST CANINE DISTEMPER, RABIES OR THE
; TITLE OF INVENTION: PARAINFLUENZA 2 VIRUS
; FILE REFERENCE: 454313-2200
; CURRENT APPLICATION NUMBER: US/09/213.053
; CURRENT FILING DATE: 1998-12-16
```

```
; EARLIER APPLICATION NUMBER: 9608242
; EARLIER FILING DATE: 1996-06-27
; EARLIER APPLICATION NUMBER: PCT/FR97/01115
; EARLIER FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide
US-09-213-053-9
```

```
Query Match      55.5%; Score 12.2; DB 3; Length 33;
Best Local Similarity 82.4%; Pred. No. 1e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      5 GACCGATATCGCTCA 21
DB      21 GATCGATATCGGCCCA 5
```

```
RESULT 17
US-09-213-053-28
; Sequence 28, Application US/09213053
; Patent No. 6159477
; GENERAL INFORMATION:
; APPLICANT: AUDONNET, Jean-Christophe
; APPLICANT: BAUDU, Philippe
; TITLE OF INVENTION: CANINE HERPESVIRUS BASED RECOMBINANT LIVE VACCINE, IN
; TITLE OF INVENTION: PARTICULAR AGAINST CANINE DISTEMPER, RABIES OR THE
; TITLE OF INVENTION: PARAINFLUENZA 2 VIRUS
; FILE REFERENCE: 454313-2200
; CURRENT APPLICATION NUMBER: US/09/213.053
; CURRENT FILING DATE: 1998-12-16
; EARLIER APPLICATION NUMBER: 9608242
; EARLIER FILING DATE: 1996-06-27
; EARLIER APPLICATION NUMBER: PCT/FR97/01115
; EARLIER FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide
US-09-213-053-28
```

```
Query Match      55.5%; Score 12.2; DB 3; Length 39;
Best Local Similarity 82.4%; Pred. No. 1e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      5 GACCGATATCGCTCA 21
DB      23 GATCGATATCGGCCCA 39
```

```
RESULT 18
US-09-213-053-28/c
; Sequence 28, Application US/09213053
; Patent No. 6159477
; GENERAL INFORMATION:
; APPLICANT: AUDONNET, Jean-Christophe
; APPLICANT: BAUDU, Philippe
; TITLE OF INVENTION: CANINE HERPESVIRUS BASED RECOMBINANT LIVE VACCINE, IN
; TITLE OF INVENTION: PARTICULAR AGAINST CANINE DISTEMPER, RABIES OR THE
; TITLE OF INVENTION: PARAINFLUENZA 2 VIRUS
; FILE REFERENCE: 454313-2200
; CURRENT APPLICATION NUMBER: US/09/213.053
```

```

; CURRENT FILING DATE: 1998-12-16
; EARLIER APPLICATION NUMBER: 9608242
; EARLIER FILING DATE: 1996-06-27
; EARLIER APPLICATION NUMBER: PCT/FR97/01115
; EARLIER FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide
US-09-213-053-28
```

```

Query Match      55.5%; Score 12.2; DB 3; Length 39;
Best Local Similarity 82.4%; Pred. No. 1e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```

QY      2 TGAGACCGATATCGGTC 18
        |||
Db      39 TGGGCCCGATATCGATC 23
```

```

RESULT 19
US-09-213-053-29
; Sequence 29, Application US/09213053
; Patent No. 6159477
; GENERAL INFORMATION:
; APPLICANT: AUDONNET, Jean-Christophe
; TITLE OF INVENTION: CANINE HERPESVIRUS BASED RECOMBINANT LIVE VACCINE, IN
; TITLE OF INVENTION: PARTICULAR AGAINST CANINE DISTEMPER, RABIES OR THE
; TITLE OF INVENTION: PARAINFLUENZA 2 VIRUS
; FILE REFERENCE: 454313-2200
; CURRENT APPLICATION NUMBER: US/09/213.053
; CURRENT FILING DATE: 1998-12-16
; EARLIER APPLICATION NUMBER: 9608242
; EARLIER FILING DATE: 1996-06-27
; EARLIER APPLICATION NUMBER: PCT/FR97/01115
; EARLIER FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide
US-09-213-053-29
```

```

Query Match      55.5%; Score 12.2; DB 3; Length 39;
Best Local Similarity 82.4%; Pred. No. 1e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```

QY      2 TGAGACCGATATCGGTC 18
        |||
Db      5 TGGGCCCGATATCGATC 21
```

```

RESULT 20
US-09-213-053-29/C
; Sequence 29, Application US/09213053
; Patent No. 6159477
; GENERAL INFORMATION:
; APPLICANT: AUDONNET, Jean-Christophe
; TITLE OF INVENTION: CANINE HERPESVIRUS BASED RECOMBINANT LIVE VACCINE, IN
; TITLE OF INVENTION: PARTICULAR AGAINST CANINE DISTEMPER, RABIES OR THE
; TITLE OF INVENTION: PARAINFLUENZA 2 VIRUS
; FILE REFERENCE: 454313-2200
```

```

; CURRENT APPLICATION NUMBER: US/09/213.053
; CURRENT FILING DATE: 1998-12-16
; EARLIER APPLICATION NUMBER: 9608242
; EARLIER FILING DATE: 1996-06-27
; EARLIER APPLICATION NUMBER: PCT/FR97/01115
; EARLIER FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide
US-09-213-053-29
```

```

Query Match      55.5%; Score 12.2; DB 3; Length 39;
Best Local Similarity 82.4%; Pred. No. 1e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```

QY      5 GACCGATATCGGTCCTCA 21
        |||
Db      21 GATCGATATCGGGCCCA 5
```

```

RESULT 21
US-08-235-503B-68
; Sequence 68, Application US/08235503B
; Patent No. 5563036
; GENERAL INFORMATION:
; APPLICANT: Peterson, Michael G
; APPLICANT: Baichwal, Vijay R
; APPLICANT: Strulovich, Berta
; TITLE OF INVENTION: TRANSCRIPTION FACTOR-DNA ASSAY
; NUMBER OF SEQUENCE ADDRESSES: 75
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: FLEHER, HOBBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/235,503B
; FILING DATE: 29-Apr-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: A-59332/RAO
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-235-503B-68
```

```

Query Match      54.5%; Score 12; DB 1; Length 28;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

OY 3 GAGACCGATATCGGTCAC 22
DB 6 CTCACACCGATTTCGGTCAC 25

RESULT 22
US-08-235-503B-68/c
Sequence 68, Application US/08235503B
Patent No. 5563036
GENERAL INFORMATION:
APPLICANT: Peterson, Michael G
APPLICANT: Balchwal, Vijay R
APPLICANT: Strulovici, Beta
TITLE OF INVENTION: TRANSCRIPTION FACTOR-DNA ASSAY
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/235,503B
FILING DATE: 29-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-59332/RAO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-235-503B-68
Query Match 54.5%; Score 12; DB 1; Length 28;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
OY 1 CTGAGACCGATATCGGTCAC 20
DB 25 CTCACACCGATTTCGGTCAC 6
RESULT 23
US-08-235-503B-69
Sequence 69, Application US/08235503B
Patent No. 5563036
GENERAL INFORMATION:
APPLICANT: Peterson, Michael G
APPLICANT: Balchwal, Vijay R
APPLICANT: Strulovici, Beta
TITLE OF INVENTION: TRANSCRIPTION FACTOR-DNA ASSAY
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA

ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/235,503B
FILING DATE: 29-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-59332/RAO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-235-503B-69
Query Match 54.5%; Score 12; DB 1; Length 28;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
OY 1 CTGAGACCGATATCGGTCAC 20
DB 4 CTCACACCGATTTCGGTCAC 23

RESULT 24
US-08-235-503B-69/c
Sequence 69, Application US/08235503B
Patent No. 5563036
GENERAL INFORMATION:
APPLICANT: Peterson, Michael G
APPLICANT: Balchwal, Vijay R
APPLICANT: Strulovici, Beta
TITLE OF INVENTION: TRANSCRIPTION FACTOR-DNA ASSAY
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/235,503B
FILING DATE: 29-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-59332/RAO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-235-503B-69

Query Match 54.5%; Score 12; DB 1; Length 28;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GAGACGATATCGGTCTCAG 22
Db 23 GTGACCGAATAACGGTGTGAG 4

RESULT 25

PCT-US95-05265-68
Sequence 68, Application PC/TUS9505265
GENERAL INFORMATION:
APPLICANT: TULARIK, INC.
TITLE OF INVENTION: TRANSCRIPTION FACTOR-DNA BINDING ASSAY
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05265
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/235,503
FILING DATE: 29-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: PP-59232-PC/RAO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
PCT-US95-05265-68

Query Match 54.5%; Score 12; DB 5; Length 28;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GAGACGATATCGGTCTCAG 22
Db 6 GTGACCGAATAACGGTGTGAG 25

RESULT 26

PCT-US95-05265-68/C
Sequence 68, Application PC/TUS9505265
GENERAL INFORMATION:
APPLICANT: TULARIK, INC.
TITLE OF INVENTION: TRANSCRIPTION FACTOR-DNA BINDING ASSAY

NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05265
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/235,503
FILING DATE: 29-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: PP-59232-PC/RAO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
PCT-US95-05265-68

Query Match 54.5%; Score 12; DB 5; Length 28;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CTGACCGATATCGGTCTC 20
Db 25 CTGACCGATATCGGTCTC 6

RESULT 27

PCT-US95-05265-69
Sequence 69, Application PC/TUS9505265
GENERAL INFORMATION:
APPLICANT: TULARIK, INC.
TITLE OF INVENTION: TRANSCRIPTION FACTOR-DNA BINDING ASSAY
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05265
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/235,503
FILING DATE: 29-APR-1994
ATTORNEY/AGENT INFORMATION:

NAME: Osman, Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: FP-59232-PC/RAO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910.277299
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
PCT-US95-05265-69

Query Match 54.5%; Score 12; DB 5; Length 28;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 1 CTGAGACGATATCGTCTC 20
Db 4 CTCACACGCTTTCGTCAC 23

RESULT 28
PCT-US95-05265-69/C
Sequence 69, Application PC/TUS9505265
GENERAL INFORMATION:
APPLICANT: TULARIK, INC.
TITLE OF INVENTION: TRANSCRIPTION FACTOR-DNA BINDING ASSAY
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOMBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05265
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/235,503
FILING DATE: 29-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: FP-59232-PC/RAO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
PCT-US95-05265-69

Query Match 54.5%; Score 12; DB 5; Length 28;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Oy 3 GAGACGATATCGTCTCAG 22

Db 23 GTGACCGAAAAACGGTGTGAG 4

RESULT 29
US-08-402-964-3
Sequence 3, Application US/08402964
Patent No. 5582993
GENERAL INFORMATION:
APPLICANT: Stackebrandt, Erko
APPLICANT: Lane, David J.
TITLE OF INVENTION: COMPOSITION AND METHODS FOR THE
DETECTION OF BACTERIA IN THE GENUS VIBRIO
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/402,964
FILING DATE: 10-MAR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/138,862
FILING DATE: 19-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/700,785
FILING DATE: 15-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Faase, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 01886/051002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-8906
TELEFAX: 617/542-5070
TELEX: 200154
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
US-08-402-964-3

Query Match 54.5%; Score 12; DB 1; Length 37;
Best Local Similarity 60.0%; Pred. No. 1.3e+03;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Oy 1 CTGAGACGATATCGTCTC 20
Db 17 CGGGAGACGAUACGGCGUC 36

RESULT 30
US-08-402-964-3/C
Sequence 3, Application US/08402964
Patent No. 5582993
GENERAL INFORMATION:
APPLICANT: Stackebrandt, Erko
APPLICANT: Lane, David J.
TITLE OF INVENTION: COMPOSITION AND METHODS FOR THE
DETECTION OF BACTERIA IN THE GENUS VIBRIO
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/402,964
FILING DATE: 10-MAR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/138,862
FILING DATE: 19-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/700,785
FILING DATE: 15-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Faese, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 01886/051002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
US-08-402-964-3

Query Match 54.5%; Score 12; DB 1; Length 37;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 GAGACCGATATCGGTCTCAG 22
|||
Db 36 GAGCCGATATCGTTCCCG 17

RESULT 31
US-09-641-638-720
Sequence 720, Application US/09641638
Patent No. 6432648
GENERAL INFORMATION:
APPLICANT: Blumenfeld, Marta
APPLICANT: Bougueleret, Lydie
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: BI-ALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
FILE REFERENCE: GENSET.051CPI
CURRENT APPLICATION NUMBER: US/09/641,638
PRIOR FILING DATE: 2000-08-16
PRIOR APPLICATION NUMBER: US 09/502,330
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: US 60/133,200
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: US 09/275,267
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: US 60/119,917
PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 1304
SOFTWARE: Patent.pm
SEQ ID NO 720
LENGTH: 47

TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: allele
LOCATION: 24
OTHER INFORMATION: 12-231-100 : polymorphic base C or T
US-09-641-638-720

Query Match 54.5%; Score 12; DB 4; Length 47;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 TGAGACCGATATCGGTCTCA 21
|||
Db 28 TTAACCGAATCGGTCTCA 47

RESULT 32
US-09-641-638-720/c
Sequence 720, Application US/09641638
Patent No. 6432648
GENERAL INFORMATION:
APPLICANT: Blumenfeld, Marta
APPLICANT: Bougueleret, Lydie
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: BI-ALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
FILE REFERENCE: GENSET.051CPI
CURRENT APPLICATION NUMBER: US/09/641,638
PRIOR FILING DATE: 2000-08-16
PRIOR APPLICATION NUMBER: US 09/502,330
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: US 60/133,200
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: US 09/275,267
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: US 60/119,917
PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 1304
SOFTWARE: Patent.pm
SEQ ID NO 720
LENGTH: 47
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: allele
LOCATION: 24
OTHER INFORMATION: 12-231-100 : polymorphic base C or T
US-09-641-638-720

Query Match 54.5%; Score 12; DB 4; Length 47;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 TGAGACCGATATCGGTCTCA 21
|||
Db 47 TGAGACCGATTCGTGTTAA 28

RESULT 33
US-09-213-053-21
Sequence 21, Application US/09213053
Patent No. 6159477
GENERAL INFORMATION:
APPLICANT: AUDONNET, Jean-Christophe
APPLICANT: BAUDU, Philippe
TITLE OF INVENTION: CANINE HERPESVIRUS BASED RECOMBINANT LIVE VACCINE, IN
TITLE OF INVENTION: PARTICULAR AGAINST CANINE DISTEMPER, RABIES OR THE
TITLE OF INVENTION: PARAINFLUENZA 2 VIRUS
FILE REFERENCE: 454313-2200
CURRENT APPLICATION NUMBER: US/09/213,053
CURRENT FILING DATE: 1998-12-16

EARLIER APPLICATION NUMBER: 9608242
EARLIER FILING DATE: 1996-06-27
EARLIER APPLICATION NUMBER: PCT/FR97/01115
EARLIER FILING DATE: 1997-06-23
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO: 21
LENGTH: 34
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
US-09-213-053-21

Query Match 53.6%; Score 11.8; DB 3; Length 34;
Best Local Similarity 86.7%; Pred. No. 1.6e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 2 TGAGACCGATATCGG 16
9 TGGGCCCGATATCGG 23

RESULT 34
US-09-213-053-21/C
Sequence 21, Application US/09213053
Patent No. 6159477
GENERAL INFORMATION:
APPLICANT: AUDONNET, Jean-Christophe
TITLE OF INVENTION: CANINE HERPESVIRUS BASED RECOMBINANT LIVE VACCINE, IN
TITLE OF INVENTION: PARTICULAR AGAINST CANINE DISTEMPER, RABIES OR THE
TITLE OF INVENTION: PARAINFLUENZA 2 VIRUS
FILE REFERENCE: 454313-2260
CURRENT APPLICATION NUMBER: US/09/213.053
CURRENT FILING DATE: 1998-12-16
EARLIER APPLICATION NUMBER: 9608242
EARLIER FILING DATE: 1996-06-27
EARLIER APPLICATION NUMBER: PCT/FR97/01115
EARLIER FILING DATE: 1997-06-23
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO: 21
LENGTH: 34
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
US-09-213-053-21

Query Match 53.6%; Score 11.8; DB 3; Length 34;
Best Local Similarity 86.7%; Pred. No. 1.6e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 7 CCGATATCGGCTCA 21
23 CCGATATCGGCGCCA 9

RESULT 35
US-07-967-693-43
Sequence 43, Application US/07967693
Patent No. 5494814
GENERAL INFORMATION:
APPLICANT: James P. Haseeloff
APPLICANT: Wayne L. Gerlach
APPLICANT: Philip A. Jennings
APPLICANT: Fiona H. Cameron
TITLE OF INVENTION: RIBOZYMES
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:

ADDRESSEE: John P. White, Esq.
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/967,693
FILING DATE: 19921027
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 40313-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-977-9550
TELEFAX: 212-664-0525
TELEX: 422523 coop ui
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
US-07-967-693-43

Query Match 53.6%; Score 11.8; DB 1; Length 45;
Best Local Similarity 80.0%; Pred. No. 1.7e+03;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 2 TGAGACCGATATCGG 16
15 UGAGUCCGATATCGG 29

RESULT 36
US-07-967-693-43/C
Sequence 43, Application US/07967693
Patent No. 5494814
GENERAL INFORMATION:
APPLICANT: James P. Haseeloff
APPLICANT: Wayne L. Gerlach
APPLICANT: Philip A. Jennings
APPLICANT: Fiona H. Cameron
TITLE OF INVENTION: RIBOZYMES
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White, Esq.
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/967,693
FILING DATE: 19921027
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 40313-B
TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-977-9550
TELEFAX: 212-664-0525
TELEX: 422523 COOP U1
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
US-07-967-693-43

Query Match 53.6%; Score 11.8; DB 1; Length 45;
Best Local Similarity 86.7%; Pred. No. 1.7e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 7 CGGATATCGGTCTCA 21
DB 29 CGGATATCGGACTCA 15

RESULT 37
US-08-195-072-41
Sequence 41, Application US/08195072
Patent No. 5543508
GENERAL INFORMATION:
APPLICANT: James P. Haseloff
APPLICANT: Wayne L. Gerlach
APPLICANT: Philip A. Jennings
APPLICANT: Fiona H. Cameron
TITLE OF INVENTION: RIBOZYMES
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White, Esq.
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/195,072
FILING DATE: 08-FEB-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 40313-G
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-977-9550
TELEFAX: 212-664-0525
TELEX: 422523 COOP U1
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
US-08-195-072-41

Query Match 53.6%; Score 11.8; DB 1; Length 45;
Best Local Similarity 80.0%; Pred. No. 1.7e+03;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 TGAGACGATATCGG 16
DB 15 UGAGUCGATATCGG 29

RESULT 38
US-08-195-072-41/c
Sequence 41, Application US/08195072
Patent No. 5543508
GENERAL INFORMATION:
APPLICANT: James P. Haseloff
APPLICANT: Wayne L. Gerlach
APPLICANT: Philip A. Jennings
APPLICANT: Fiona H. Cameron
TITLE OF INVENTION: RIBOZYMES
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White, Esq.
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/195,072
FILING DATE: 08-FEB-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 40313-G
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-977-9550
TELEFAX: 212-664-0525
TELEX: 422523 COOP U1
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
US-08-195-072-41

Query Match 53.6%; Score 11.8; DB 1; Length 45;
Best Local Similarity 86.7%; Pred. No. 1.7e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 29 CGGATATCGGACTCA 15

RESULT 39
US-08-195-735-41
Sequence 41, Application US/08195735
Patent No. 5574143
GENERAL INFORMATION:
APPLICANT: James P. Haseloff
APPLICANT: Wayne L. Gerlach
APPLICANT: Philip A. Jennings
APPLICANT: Fiona H. Cameron
TITLE OF INVENTION: RIBOZYMES
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White, Esq.
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:

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: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/195,735
: FILING DATE: 08-FEB-1994
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: White, John P.
: REGISTRATION NUMBER: 28,678
: REFERENCE/DOCKET NUMBER: 40313-E
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 212-977-9550
: TELEFAX: 212-664-0525
: TELEX: 422523 COOP U1
: INFORMATION FOR SEQ ID NO: 41:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 45 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: RNA (genomic)
: US-08-195-735-41

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Best Local Similarity 80.0%; Pred. No. 1.7e+03;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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RESULT 40
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: Sequence 41, Application US/08195735
: Patent No. 5574143
: GENERAL INFORMATION:
: APPLICANT: James P. Haseloff
: APPLICANT: Wayne L. Gerlach
: APPLICANT: Philip A. Jennings
: APPLICANT: Fiona H. Cameron
: TITLE OF INVENTION: RIBOZYMES
: NUMBER OF SEQUENCES: 44
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: John P. White, Esq.
: STREET: 30 Rockefeller Plaza
: CITY: New York
: STATE: New York
: COUNTRY: USA
: ZIP: 10112

COMPUTER READABLE FORM:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/195,735
FILING DATE: 08-FEB-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 40313-E
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-977-9550
TELEFAX: 212-664-0525
TELEX: 422523 COOP U1
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid

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: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: RNA (genomic)
: US-08-195-735-41

Query Match      53.6%; Score 11.8; DB 1; Length 45;
Best Local Similarity 86.7%; Pred. No. 1.7e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Perfect score: 22
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Searched: 1029858 seqs, 724030393 residues

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Listing first 1000 summaries

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Published Applications_NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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139	11.4	51.8	25	9	US-10-098-263B-35948	Sequence 35948, A	c 212	11.2	50.9	25	9	US-10-098-263B-103599	Sequence 103599, A
140	11.4	51.8	25	9	US-10-098-263B-35948	Sequence 35948, A	c 213	11.2	50.9	33	9	US-09-900-590-43	Sequence 43, Appl
141	11.4	51.8	25	9	US-10-098-263B-83126	Sequence 83126, A	c 214	11.2	50.9	33	9	US-09-900-590-43	Sequence 43, Appl
142	11.4	51.8	25	9	US-10-098-263B-83126	Sequence 83126, A	c 215	11.2	50.9	38	9	US-09-877-478-1621	Sequence 3621, Ap
143	11.4	51.8	25	9	US-10-098-263B-88699	Sequence 88699, A	c 216	11.2	50.9	38	9	US-09-877-478-1621	Sequence 3621, Ap
144	11.4	51.8	25	9	US-10-098-263B-88699	Sequence 88699, A	c 217	11.2	50.9	20	10	US-09-441-522-14	Sequence 14, Appl
145	11.4	51.8	25	9	US-10-098-263B-101532	Sequence 101532, A	c 218	11.2	50.9	20	10	US-09-441-522-14	Sequence 14, Appl
146	11.4	51.8	25	9	US-10-098-263B-101532	Sequence 101532, A	c 219	11.2	50.9	25	9	US-10-215-112-1277	Sequence 3377, Ap
147	11.4	51.8	25	9	US-10-098-263B-118692	Sequence 118692, A	c 220	11.2	50.9	25	9	US-10-215-112-1277	Sequence 3377, Ap
148	11.4	51.8	25	9	US-10-098-263B-118692	Sequence 118692, A	c 221	11.2	50.9	25	9	US-10-215-112-5279	Sequence 5279, Ap
149	11.4	51.8	25	9	US-10-098-263B-123691	Sequence 123691, A	c 222	11.2	50.9	25	9	US-10-215-112-5279	Sequence 5279, Ap
150	11.4	51.8	25	9	US-10-098-263B-123691	Sequence 123691, A	c 223	11.2	50.9	25	9	US-10-215-112-5405	Sequence 5405, Ap
151	11.4	51.8	25	9	US-10-098-263B-127919	Sequence 127919, A	c 224	11.2	50.9	25	9	US-10-215-112-5405	Sequence 5405, Ap
152	11.4	51.8	25	9	US-10-098-263B-127919	Sequence 127919, A	c 225	11.2	50.9	25	9	US-10-215-112-10771	Sequence 10771, A
153	11.4	51.8	29	10	US-09-893-615-84	Sequence 84, Appl	c 226	11.2	50.9	25	9	US-10-215-112-10771	Sequence 10771, A
154	11.4	51.8	29	10	US-09-893-615-84	Sequence 84, Appl	c 227	11.2	50.9	25	9	US-10-215-112-12780	Sequence 12780, A
155	11.4	51.8	29	10	US-09-753-126-54	Sequence 54, Appl	c 228	11.2	50.9	25	9	US-10-215-112-12780	Sequence 12780, A
156	11.4	51.8	29	10	US-09-753-126-54	Sequence 54, Appl	c 229	11.2	50.9	25	9	US-09-940-185-4107	Sequence 4107, Ap
157	11.4	51.8	38	9	US-09-966-277-37	Sequence 37, Appl	c 230	11.2	50.9	25	9	US-09-940-185-4107	Sequence 4107, Ap
158	11.4	51.8	38	9	US-09-966-277-37	Sequence 37, Appl	c 231	11.2	50.9	25	9	US-10-098-263B-6851	Sequence 6851, Ap
159	11.4	51.8	38	9	US-09-966-277-38	Sequence 38, Appl	c 232	11.2	50.9	25	9	US-10-098-263B-6851	Sequence 6851, Ap
160	11.4	51.8	38	9	US-09-966-277-38	Sequence 38, Appl	c 233	11.2	50.9	25	9	US-10-098-263B-6852	Sequence 6852, Ap
161	11.4	51.8	38	9	US-09-966-930-37	Sequence 37, Appl	c 234	11.2	50.9	25	9	US-10-098-263B-6852	Sequence 6852, Ap
162	11.4	51.8	38	9	US-09-966-930-37	Sequence 37, Appl	c 235	11.2	50.9	25	9	US-10-098-263B-7487	Sequence 7487, Ap
163	11.4	51.8	38	9	US-09-966-930-38	Sequence 38, Appl	c 236	11.2	50.9	25	9	US-10-098-263B-7487	Sequence 7487, Ap
164	11.4	51.8	38	9	US-09-966-930-38	Sequence 38, Appl	c 237	11.2	50.9	25	9	US-10-098-263B-7488	Sequence 7488, Ap
165	11.4	51.8	39	9	US-09-824-017-15	Sequence 15, Appl	c 238	11.2	50.9	25	9	US-10-098-263B-7488	Sequence 7488, Ap

C 239	11	50.0	25	9	US-10-098-263B-10947	Sequence 10947, A	C 312	10.8	49.1	25	9	US-10-098-263B-19329	Sequence 19329, A
C 240	11	50.0	25	9	US-10-098-263B-10947	Sequence 10947, A	C 313	10.8	49.1	25	9	US-10-098-263B-21860	Sequence 21860, A
C 241	11	50.0	25	9	US-10-098-263B-10948	Sequence 10948, A	C 314	10.8	49.1	25	9	US-10-098-263B-21860	Sequence 21860, A
C 242	11	50.0	25	9	US-10-098-263B-10948	Sequence 10948, A	C 315	10.8	49.1	25	9	US-10-098-263B-25767	Sequence 25767, A
C 243	11	50.0	25	9	US-10-098-263B-14534	Sequence 14534, A	C 316	10.8	49.1	25	9	US-10-098-263B-25767	Sequence 25767, A
C 244	11	50.0	25	9	US-10-098-263B-14534	Sequence 14534, A	C 317	10.8	49.1	25	9	US-10-098-263B-26347	Sequence 26347, A
C 245	11	50.0	25	9	US-10-098-263B-17340	Sequence 17340, A	C 318	10.8	49.1	25	9	US-10-098-263B-26947	Sequence 26947, A
C 246	11	50.0	25	9	US-10-098-263B-17340	Sequence 17340, A	C 319	10.8	49.1	25	9	US-10-098-263B-28731	Sequence 28731, A
C 247	11	50.0	25	9	US-10-098-263B-19137	Sequence 19137, A	C 320	10.8	49.1	25	9	US-10-098-263B-35938	Sequence 35938, A
C 248	11	50.0	25	9	US-10-098-263B-19137	Sequence 19137, A	C 321	10.8	49.1	25	9	US-10-098-263B-35938	Sequence 35938, A
C 249	11	50.0	25	9	US-10-098-263B-23785	Sequence 23785, A	C 322	10.8	49.1	25	9	US-10-098-263B-35938	Sequence 35938, A
C 250	11	50.0	25	9	US-10-098-263B-23785	Sequence 23785, A	C 323	10.8	49.1	25	9	US-10-098-263B-48087	Sequence 48087, A
C 251	11	50.0	25	9	US-10-098-263B-52290	Sequence 52290, A	C 324	10.8	49.1	25	9	US-10-098-263B-48087	Sequence 48087, A
C 252	11	50.0	25	9	US-10-098-263B-52290	Sequence 52290, A	C 325	10.8	49.1	25	9	US-10-098-263B-48255	Sequence 48255, A
C 253	11	50.0	25	9	US-10-098-263B-52785	Sequence 52785, A	C 326	10.8	49.1	25	9	US-10-098-263B-48255	Sequence 48255, A
C 254	11	50.0	25	9	US-10-098-263B-52785	Sequence 52785, A	C 327	10.8	49.1	25	9	US-10-098-263B-53591	Sequence 53591, A
C 255	11	50.0	25	9	US-10-098-263B-57224	Sequence 57224, A	C 328	10.8	49.1	25	9	US-10-098-263B-53591	Sequence 53591, A
C 256	11	50.0	25	9	US-10-098-263B-57224	Sequence 57224, A	C 329	10.8	49.1	25	9	US-10-098-263B-53831	Sequence 53831, A
C 257	11	50.0	25	9	US-10-098-263B-63312	Sequence 63312, A	C 330	10.8	49.1	25	9	US-10-098-263B-53831	Sequence 53831, A
C 258	11	50.0	25	9	US-10-098-263B-63312	Sequence 63312, A	C 331	10.8	49.1	25	9	US-10-098-263B-61572	Sequence 61572, A
C 259	11	50.0	25	9	US-10-098-263B-64811	Sequence 64811, A	C 332	10.8	49.1	25	9	US-10-098-263B-61572	Sequence 61572, A
C 260	11	50.0	25	9	US-10-098-263B-64811	Sequence 64811, A	C 333	10.8	49.1	25	9	US-10-098-263B-61862	Sequence 61862, A
C 261	11	50.0	25	9	US-10-098-263B-66051	Sequence 66051, A	C 334	10.8	49.1	25	9	US-10-098-263B-61862	Sequence 61862, A
C 262	11	50.0	25	9	US-10-098-263B-66051	Sequence 66051, A	C 335	10.8	49.1	25	9	US-10-098-263B-63695	Sequence 63695, A
C 263	11	50.0	25	9	US-10-098-263B-66052	Sequence 66052, A	C 336	10.8	49.1	25	9	US-10-098-263B-63695	Sequence 63695, A
C 264	11	50.0	25	9	US-10-098-263B-66052	Sequence 66052, A	C 337	10.8	49.1	25	9	US-10-098-263B-74524	Sequence 74524, A
C 265	11	50.0	25	9	US-10-098-263B-68684	Sequence 68684, A	C 338	10.8	49.1	25	9	US-10-098-263B-74524	Sequence 74524, A
C 266	11	50.0	25	9	US-10-098-263B-68684	Sequence 68684, A	C 339	10.8	49.1	25	9	US-10-098-263B-79851	Sequence 79851, A
C 267	11	50.0	25	9	US-10-098-263B-71442	Sequence 71442, A	C 340	10.8	49.1	25	9	US-10-098-263B-79851	Sequence 79851, A
C 268	11	50.0	25	9	US-10-098-263B-71442	Sequence 71442, A	C 341	10.8	49.1	25	9	US-10-098-263B-99205	Sequence 99205, A
C 269	11	50.0	25	9	US-10-098-263B-72969	Sequence 72969, A	C 342	10.8	49.1	25	9	US-10-098-263B-99205	Sequence 99205, A
C 270	11	50.0	25	9	US-10-098-263B-72969	Sequence 72969, A	C 343	10.8	49.1	25	9	US-10-098-263B-101400	Sequence 101400, A
C 271	11	50.0	25	9	US-10-098-263B-87337	Sequence 87337, A	C 344	10.8	49.1	25	9	US-10-098-263B-101400	Sequence 101400, A
C 272	11	50.0	25	9	US-10-098-263B-87337	Sequence 87337, A	C 345	10.8	49.1	25	9	US-10-098-263B-101571	Sequence 101571, A
C 273	11	50.0	25	9	US-10-098-263B-87338	Sequence 87338, A	C 346	10.8	49.1	25	9	US-10-098-263B-101571	Sequence 101571, A
C 274	11	50.0	25	9	US-10-098-263B-87338	Sequence 87338, A	C 347	10.8	49.1	25	9	US-10-098-263B-107450	Sequence 107450, A
C 275	11	50.0	25	9	US-10-098-263B-101699	Sequence 101699, A	C 348	10.8	49.1	25	9	US-10-098-263B-107450	Sequence 107450, A
C 276	11	50.0	25	9	US-10-098-263B-101699	Sequence 101699, A	C 349	10.8	49.1	25	9	US-10-098-263B-109684	Sequence 109684, A
C 277	11	50.0	25	9	US-10-098-263B-101700	Sequence 101700, A	C 350	10.8	49.1	25	9	US-10-098-263B-109684	Sequence 109684, A
C 278	11	50.0	25	9	US-10-098-263B-101700	Sequence 101700, A	C 351	10.8	49.1	25	9	US-10-098-263B-110252	Sequence 110252, A
C 279	11	50.0	25	9	US-10-098-263B-115034	Sequence 115034, A	C 352	10.8	49.1	25	9	US-10-098-263B-110252	Sequence 110252, A
C 280	11	50.0	25	9	US-10-098-263B-115034	Sequence 115034, A	C 353	10.8	49.1	25	9	US-10-098-263B-124541	Sequence 124541, A
C 281	11	50.0	25	9	US-10-098-263B-120179	Sequence 120179, A	C 354	10.8	49.1	25	9	US-10-098-263B-124541	Sequence 124541, A
C 282	11	50.0	25	9	US-10-098-263B-120179	Sequence 120179, A	C 355	10.8	49.1	25	9	US-10-098-263B-124542	Sequence 124542, A
C 283	11	50.0	25	9	US-10-098-263B-120180	Sequence 120180, A	C 356	10.8	49.1	25	9	US-10-098-263B-124542	Sequence 124542, A
C 284	11	50.0	25	9	US-10-098-263B-120180	Sequence 120180, A	C 357	10.8	49.1	25	9	US-10-098-263B-125766	Sequence 125766, A
C 285	11	50.0	25	9	US-10-098-263B-121579	Sequence 121579, A	C 358	10.8	49.1	25	9	US-10-098-263B-125766	Sequence 125766, A
C 286	11	50.0	25	9	US-10-098-263B-121579	Sequence 121579, A	C 359	10.8	49.1	32	9	US-10-282-602-5	Sequence 5, Appl1
C 287	11	50.0	25	9	US-10-098-263B-121584	Sequence 121584, A	C 360	10.8	49.1	32	9	US-10-282-602-5	Sequence 5, Appl1
C 288	11	50.0	25	9	US-10-098-263B-121684	Sequence 121684, A	C 361	10.8	49.1	35	9	US-10-194-594-3	Sequence 3, Appl1
C 289	11	50.0	25	9	US-10-098-263B-121684	Sequence 121684, A	C 362	10.8	49.1	35	9	US-10-194-594-3	Sequence 3, Appl1
C 290	11	50.0	25	9	US-10-098-263B-129558	Sequence 129558, A	C 363	10.8	49.1	38	9	US-09-997-488A-3	Sequence 3, Appl1
C 291	11	50.0	25	9	US-10-098-263B-129558	Sequence 129558, A	C 364	10.8	49.1	38	9	US-09-997-488A-3	Sequence 3, Appl1
C 292	11	50.0	25	9	US-10-098-263B-130374	Sequence 130374, A	C 365	10.8	49.1	48	10	US-09-464-767A-2	Sequence 2, Appl1
C 293	11	50.0	37	9	US-10-036-949-56	Sequence 56, Appl1	C 366	10.8	48.2	17	9	US-09-464-767A-2	Sequence 2, Appl1
C 294	11	50.0	37	9	US-10-036-949-56	Sequence 56, Appl1	C 367	10.6	48.2	17	9	US-09-864-636A-1830	Sequence 1830, Ap1
C 295	11	50.0	37	9	US-10-002-720-9	Sequence 9, Appl1	C 368	10.6	48.2	17	9	US-09-864-636A-1830	Sequence 1830, Ap1
C 296	11	50.0	37	9	US-10-002-720-9	Sequence 9, Appl1	C 369	10.6	48.2	20	10	US-09-735-995-86	Sequence 86, Appl1
C 297	11	50.0	38	9	US-10-235-618A-7	Sequence 7, Appl1	C 370	10.6	48.2	20	10	US-09-735-995-86	Sequence 86, Appl1
C 298	11	50.0	38	9	US-10-235-618A-7	Sequence 7, Appl1	C 371	10.6	48.2	24	9	US-09-940-185-1243	Sequence 1243, Ap
C 299	11	50.0	46	9	US-09-860-738C-75	Sequence 75, Appl1	C 372	10.6	48.2	24	9	US-09-940-185-1243	Sequence 1243, Ap
C 300	11	50.0	46	9	US-09-860-738C-75	Sequence 75, Appl1	C 373	10.6	48.2	24	9	US-10-011-855-3	Sequence 3, Appl1
C 301	11	50.0	46	9	US-09-860-738C-80	Sequence 80, Appl1	C 374	10.6	48.2	24	9	US-10-011-855-3	Sequence 3, Appl1
C 302	11	50.0	46	9	US-09-860-738C-80	Sequence 80, Appl1	C 375	10.6	48.2	24	9	US-10-011-855-7	Sequence 7, Appl1
C 303	11	50.0	48	9	US-09-938-433-15	Sequence 15, Appl1	C 376	10.6	48.2	24	9	US-10-011-855-7	Sequence 7, Appl1
C 304	11	50.0	48	9	US-09-938-433-15	Sequence 15, Appl1	C 377	10.6	48.2	25	9	US-10-215-112-735	Sequence 75, App
C 305	11	50.0	48	10	US-09-788-209A-15	Sequence 15, Appl1	C 378	10.6	48.2	25	9	US-10-215-112-735	Sequence 75, App
C 306	11	50.0	48	10	US-09-788-209A-15	Sequence 15, Appl1	C 379	10.6	48.2	25	9	US-10-215-112-3251	Sequence 2251, Ap
C 307	10.8	49.1	25	9	US-10-215-112-4731	Sequence 4731, Ap	C 380	10.6	48.2	25	9	US-10-215-112-3251	Sequence 2251, Ap
C 308	10.8	49.1	25	9	US-10-215-112-4731	Sequence 4731, Ap	C 381	10.6	48.2	25	9	US-10-215-112-3701	Sequence 3701, Ap
C 309	10.8	49.1	25	9	US-10-215-112-10329	Sequence 10329, A	C 382	10.6	48.2	25	9	US-10-215-112-3701	Sequence 3701, Ap
C 310	10.8	49.1	25	9	US-10-215-112-10329	Sequence 10329, A	C 383	10.6	48.2	25	9	US-10-215-112-14421	Sequence 14421, A
C 311	10.8	49.1	25	9	US-10-098-263B-19329	Sequence 19329, A	C 384	10.6	48.2	25	9	US-10-215-112-14421	Sequence 14421, A

385	10.6	48.2	25	9	US-10-098-263B-2312	Sequence 2312, Ap	C 458	10.6	48.2	25	9	US-10-098-263B-114619	Sequence 114619, Ap
386	10.6	48.2	25	9	US-10-098-263B-2312	Sequence 2312, Ap	C 459	10.6	48.2	25	9	US-10-098-263B-114620	Sequence 114620, Ap
387	10.6	48.2	25	9	US-10-098-263B-5243	Sequence 5243, Ap	C 460	10.6	48.2	25	9	US-10-098-263B-114620	Sequence 114620, Ap
388	10.6	48.2	25	9	US-10-098-263B-5243	Sequence 5243, Ap	C 461	10.6	48.2	25	9	US-10-098-263B-114799	Sequence 114799, Ap
389	10.6	48.2	25	9	US-10-098-263B-13026	Sequence 13026, Ap	C 462	10.6	48.2	25	9	US-10-098-263B-114799	Sequence 114799, Ap
390	10.6	48.2	25	9	US-10-098-263B-13026	Sequence 13026, Ap	C 463	10.6	48.2	25	9	US-10-098-263B-114800	Sequence 114800, Ap
391	10.6	48.2	25	9	US-10-098-263B-15179	Sequence 15179, A	C 464	10.6	48.2	25	9	US-10-098-263B-114800	Sequence 114800, Ap
392	10.6	48.2	25	9	US-10-098-263B-15179	Sequence 15179, A	C 465	10.6	48.2	25	9	US-10-098-263B-115255	Sequence 115255, Ap
393	10.6	48.2	25	9	US-10-098-263B-17254	Sequence 17254, A	C 466	10.6	48.2	25	9	US-10-098-263B-115255	Sequence 115255, Ap
394	10.6	48.2	25	9	US-10-098-263B-17254	Sequence 17254, A	C 467	10.6	48.2	25	9	US-10-098-263B-115256	Sequence 115256, Ap
395	10.6	48.2	25	9	US-10-098-263B-27743	Sequence 27743, A	C 468	10.6	48.2	25	9	US-10-098-263B-115256	Sequence 115256, Ap
396	10.6	48.2	25	9	US-10-098-263B-27743	Sequence 27743, A	C 469	10.6	48.2	25	9	US-10-098-263B-119017	Sequence 119017, Ap
397	10.6	48.2	25	9	US-10-098-263B-36953	Sequence 36953, A	C 470	10.6	48.2	25	9	US-10-098-263B-119017	Sequence 119017, Ap
398	10.6	48.2	25	9	US-10-098-263B-36953	Sequence 36953, A	C 471	10.6	48.2	25	9	US-10-098-263B-120718	Sequence 120718, Ap
399	10.6	48.2	25	9	US-10-098-263B-37937	Sequence 37937, A	C 472	10.6	48.2	25	9	US-10-098-263B-120718	Sequence 120718, Ap
400	10.6	48.2	25	9	US-10-098-263B-37937	Sequence 37937, A	C 473	10.6	48.2	25	9	US-10-098-263B-126450	Sequence 126450, Ap
401	10.6	48.2	25	9	US-10-098-263B-38165	Sequence 38165, A	C 474	10.6	48.2	25	9	US-10-098-263B-126450	Sequence 126450, Ap
402	10.6	48.2	25	9	US-10-098-263B-38165	Sequence 38165, A	C 475	10.6	48.2	25	9	US-10-098-263B-127345	Sequence 127345, Ap
403	10.6	48.2	25	9	US-10-098-263B-55643	Sequence 55643, A	C 476	10.6	48.2	25	9	US-10-098-263B-127345	Sequence 127345, Ap
404	10.6	48.2	25	9	US-10-098-263B-55643	Sequence 55643, A	C 477	10.6	48.2	25	9	US-10-098-263B-127346	Sequence 127346, Ap
405	10.6	48.2	25	9	US-10-098-263B-55644	Sequence 55644, A	C 478	10.6	48.2	25	9	US-10-098-263B-127346	Sequence 127346, Ap
406	10.6	48.2	25	9	US-10-098-263B-55644	Sequence 55644, A	C 479	10.6	48.2	25	9	US-10-098-263B-128488	Sequence 128488, Ap
407	10.6	48.2	25	9	US-10-098-263B-58373	Sequence 58373, A	C 480	10.6	48.2	25	9	US-10-098-263B-128488	Sequence 128488, Ap
408	10.6	48.2	25	9	US-10-098-263B-58373	Sequence 58373, A	C 481	10.6	48.2	25	9	US-10-098-263B-128879	Sequence 128879, Ap
409	10.6	48.2	25	9	US-10-098-263B-58374	Sequence 58374, A	C 482	10.6	48.2	25	9	US-10-098-263B-128879	Sequence 128879, Ap
410	10.6	48.2	25	9	US-10-098-263B-58374	Sequence 58374, A	C 483	10.6	48.2	25	9	US-10-098-263B-128880	Sequence 128880, Ap
411	10.6	48.2	25	9	US-10-098-263B-65152	Sequence 65152, A	C 484	10.6	48.2	25	9	US-10-098-263B-128880	Sequence 128880, Ap
412	10.6	48.2	25	9	US-10-098-263B-65152	Sequence 65152, A	C 485	10.6	48.2	30	9	US-10-011-635A-4	Sequence 4, Appl1
413	10.6	48.2	25	9	US-10-098-263B-66667	Sequence 66667, A	C 486	10.6	48.2	30	9	US-10-011-635A-4	Sequence 4, Appl1
414	10.6	48.2	25	9	US-10-098-263B-66667	Sequence 66667, A	C 487	10.6	48.2	31	9	US-10-011-721-B	Sequence 8, Appl1
415	10.6	48.2	25	9	US-10-098-263B-67925	Sequence 67925, A	C 488	10.6	48.2	31	9	US-10-011-721-B	Sequence 8, Appl1
416	10.6	48.2	25	9	US-10-098-263B-67925	Sequence 67925, A	C 489	10.6	48.2	34	9	US-10-138-838-A	Sequence 4, Appl1
417	10.6	48.2	25	9	US-10-098-263B-67926	Sequence 67926, A	C 490	10.6	48.2	34	9	US-10-138-838-A	Sequence 4, Appl1
418	10.6	48.2	25	9	US-10-098-263B-67926	Sequence 67926, A	C 491	10.6	48.2	34	9	US-10-138-838-A	Sequence 4, Appl1
419	10.6	48.2	25	9	US-10-098-263B-68013	Sequence 68013, A	C 492	10.6	48.2	34	9	US-10-138-838-A	Sequence 4, Appl1
420	10.6	48.2	25	9	US-10-098-263B-68013	Sequence 68013, A	C 493	10.6	48.2	34	9	US-10-138-905-A	Sequence 4, Appl1
421	10.6	48.2	25	9	US-10-098-263B-68170	Sequence 68170, A	C 494	10.6	48.2	34	9	US-10-138-905-A	Sequence 4, Appl1
422	10.6	48.2	25	9	US-10-098-263B-68170	Sequence 68170, A	C 495	10.6	48.2	34	9	US-10-138-916-A	Sequence 4, Appl1
423	10.6	48.2	25	9	US-10-098-263B-75129	Sequence 75129, A	C 496	10.6	48.2	34	9	US-10-138-916-A	Sequence 4, Appl1
424	10.6	48.2	25	9	US-10-098-263B-75129	Sequence 75129, A	C 497	10.6	48.2	34	9	US-09-976-800-A	Sequence 4, Appl1
425	10.6	48.2	25	9	US-10-098-263B-75130	Sequence 75130, A	C 498	10.6	48.2	34	9	US-09-976-800-A	Sequence 4, Appl1
426	10.6	48.2	25	9	US-10-098-263B-75130	Sequence 75130, A	C 499	10.6	48.2	34	9	US-10-234-007-18	Sequence 18, Appl1
427	10.6	48.2	25	9	US-10-098-263B-75663	Sequence 75663, A	C 500	10.6	48.2	34	9	US-09-504-231A-1767	Sequence 16, Appl1
428	10.6	48.2	25	9	US-10-098-263B-75663	Sequence 75663, A	C 501	10.6	48.2	36	10	US-09-504-231A-1767	Sequence 16, Appl1
429	10.6	48.2	25	9	US-10-098-263B-75998	Sequence 75998, A	C 502	10.6	48.2	36	10	US-09-504-231A-2403	Sequence 2403, Ap
430	10.6	48.2	25	9	US-10-098-263B-75998	Sequence 75998, A	C 503	10.6	48.2	36	10	US-09-504-231A-2403	Sequence 2403, Ap
431	10.6	48.2	25	9	US-10-098-263B-81003	Sequence 81003, A	C 504	10.6	48.2	36	10	US-09-504-231A-2403	Sequence 2403, Ap
432	10.6	48.2	25	9	US-10-098-263B-81003	Sequence 81003, A	C 505	10.6	48.2	36	10	US-09-274-553D-1767	Sequence 1767, Ap
433	10.6	48.2	25	9	US-10-098-263B-81450	Sequence 81450, A	C 506	10.6	48.2	36	10	US-09-274-553D-1767	Sequence 1767, Ap
434	10.6	48.2	25	9	US-10-098-263B-81450	Sequence 81450, A	C 507	10.6	48.2	36	10	US-09-274-553D-1767	Sequence 1767, Ap
435	10.6	48.2	25	9	US-10-098-263B-82989	Sequence 82989, A	C 508	10.6	48.2	36	10	US-09-274-553D-2403	Sequence 2403, Ap
436	10.6	48.2	25	9	US-10-098-263B-82989	Sequence 82989, A	C 509	10.6	48.2	37	10	US-09-778-168-16	Sequence 16, Appl1
437	10.6	48.2	25	9	US-10-098-263B-83528	Sequence 83528, A	C 510	10.6	48.2	37	10	US-09-778-168-16	Sequence 16, Appl1
438	10.6	48.2	25	9	US-10-098-263B-83528	Sequence 83528, A	C 511	10.6	48.2	37	10	US-09-778-175-16	Sequence 16, Appl1
439	10.6	48.2	25	9	US-10-098-263B-84097	Sequence 84097, A	C 512	10.6	48.2	37	10	US-09-778-175-16	Sequence 16, Appl1
440	10.6	48.2	25	9	US-10-098-263B-84097	Sequence 84097, A	C 513	10.6	48.2	37	10	US-09-335-218-16	Sequence 16, Appl1
441	10.6	48.2	25	9	US-10-098-263B-86270	Sequence 86270, A	C 514	10.6	48.2	37	10	US-09-335-218-16	Sequence 16, Appl1
442	10.6	48.2	25	9	US-10-098-263B-86270	Sequence 86270, A	C 515	10.6	48.2	38	9	US-09-846-785-754	Sequence 754, Appl1
443	10.6	48.2	25	9	US-10-098-263B-90294	Sequence 90294, A	C 516	10.6	48.2	38	9	US-09-846-785-754	Sequence 754, Appl1
444	10.6	48.2	25	9	US-10-098-263B-90294	Sequence 90294, A	C 517	10.6	48.2	38	9	US-09-846-785-824	Sequence 824, Appl1
445	10.6	48.2	25	9	US-10-098-263B-90837	Sequence 90837, A	C 518	10.6	48.2	38	9	US-09-846-785-824	Sequence 824, Appl1
446	10.6	48.2	25	9	US-10-098-263B-90837	Sequence 90837, A	C 519	10.6	48.2	38	9	US-09-780-533A-3220	Sequence 3220, Ap
447	10.6	48.2	25	9	US-10-098-263B-99766	Sequence 99766, A	C 520	10.6	48.2	38	9	US-09-780-533A-3220	Sequence 3220, Ap
448	10.6	48.2	25	9	US-10-098-263B-99766	Sequence 99766, A	C 521	10.6	48.2	38	9	US-09-846-754A-3897	Sequence 3897, Ap
449	10.6	48.2	25	9	US-10-098-263B-103541	Sequence 103541, A	C 522	10.6	48.2	38	9	US-09-846-754A-3897	Sequence 3897, Ap
450	10.6	48.2	25	9	US-10-098-263B-103541	Sequence 103541, A	C 523	10.6	48.2	38	9	US-09-846-754A-4106	Sequence 4106, Ap
451	10.6	48.2	25	9	US-10-098-263B-105403	Sequence 105403, A	C 524	10.6	48.2	38	9	US-09-846-754A-4106	Sequence 4106, Ap
452	10.6	48.2	25	9	US-10-098-263B-105403	Sequence 105403, A	C 525	10.6	48.2	38	9	US-09-846-754A-4397	Sequence 4397, Ap
453	10.6	48.2	25	9	US-10-098-263B-108259	Sequence 108259, A	C 526	10.6	48.2	38	9	US-09-846-754A-4397	Sequence 4397, Ap
454	10.6	48.2	25	9	US-10-098-263B-108259	Sequence 108259, A	C 527	10.6	48.2	38	9	US-09-846-754A-4817	Sequence 4817, Ap
455	10.6	48.2	25	9	US-10-098-263B-113887	Sequence 113887, A	C 528	10.6	48.2	38	9	US-09-846-754A-4817	Sequence 4817, Ap
456	10.6	48.2	25	9	US-10-098-263B-113887	Sequence 113887, A	C 529	10.6	48.2	38	9	US-09-846-754A-5441	Sequence 5441, Ap
457	10.6	48.2	25	9	US-10-098-263B-114619	Sequence 114619, A	C 530	10.6	48.2	38	9	US-09-846-754A-5441	Sequence 5441, Ap

C 531	10.6	48.2	38	9	US-09-848-754A-5559	Sequence 5559, Ap	C 604	10.4	47.3	25	9	US-10-098-263B-32766	Sequence 32766, A
C 532	10.6	48.2	38	9	US-09-848-754A-5559	Sequence 5559, Ap	C 605	10.4	47.3	25	9	US-10-098-263B-35411	Sequence 35411, A
C 533	10.6	48.2	38	9	US-09-848-754A-5564	Sequence 5564, Ap	C 606	10.4	47.3	25	9	US-10-098-263B-35411	Sequence 35411, A
C 534	10.6	48.2	38	9	US-09-848-754A-5564	Sequence 5564, Ap	C 607	10.4	47.3	25	9	US-10-098-263B-35412	Sequence 35412, A
C 535	10.6	48.2	38	9	US-09-848-754A-5567	Sequence 5567, Ap	C 608	10.4	47.3	25	9	US-10-098-263B-35412	Sequence 35412, A
C 536	10.6	48.2	38	9	US-09-848-754A-5687	Sequence 5687, Ap	C 609	10.4	47.3	25	9	US-10-098-263B-35900	Sequence 35900, A
C 537	10.6	48.2	38	9	US-09-930-423-1790	Sequence 1790, Ap	C 610	10.4	47.3	25	9	US-10-098-263B-35900	Sequence 35900, A
C 538	10.6	48.2	38	9	US-09-930-423-1790	Sequence 1790, Ap	C 611	10.4	47.3	25	9	US-10-098-263B-36490	Sequence 36490, A
C 539	10.6	48.2	38	10	US-09-904-621-5	Sequence 5, Appl1	C 612	10.4	47.3	25	9	US-10-098-263B-36490	Sequence 36490, A
C 540	10.6	48.2	38	10	US-09-904-621-5	Sequence 5, Appl1	C 613	10.4	47.3	25	9	US-10-098-263B-44740	Sequence 44740, A
C 541	10.6	48.2	39	9	US-09-500-700-46	Sequence 46, Appl1	C 614	10.4	47.3	25	9	US-10-098-263B-44740	Sequence 44740, A
C 542	10.6	48.2	39	9	US-09-500-700-46	Sequence 46, Appl1	C 615	10.4	47.3	25	9	US-10-098-263B-57750	Sequence 57750, A
C 543	10.6	48.2	43	9	US-10-193-960-57	Sequence 57, Appl1	C 616	10.4	47.3	25	9	US-10-098-263B-57750	Sequence 57750, A
C 544	10.6	48.2	43	9	US-10-193-960-57	Sequence 57, Appl1	C 617	10.4	47.3	25	9	US-10-098-263B-58103	Sequence 58103, A
C 545	10.6	48.2	44	10	US-09-896-888A-2	Sequence 2, Appl1	C 618	10.4	47.3	25	9	US-10-098-263B-58103	Sequence 58103, A
C 546	10.6	48.2	44	10	US-09-896-888A-2	Sequence 2, Appl1	C 619	10.4	47.3	25	9	US-10-098-263B-62610	Sequence 62610, A
C 547	10.6	48.2	45	9	US-10-007-132-12	Sequence 12, Appl1	C 620	10.4	47.3	25	9	US-10-098-263B-62610	Sequence 62610, A
C 548	10.6	48.2	45	9	US-10-007-132-12	Sequence 12, Appl1	C 621	10.4	47.3	25	9	US-10-098-263B-62772	Sequence 62772, A
C 549	10.6	48.2	45	9	US-09-771-287-12	Sequence 12, Appl1	C 622	10.4	47.3	25	9	US-10-098-263B-62772	Sequence 62772, A
C 550	10.6	48.2	45	9	US-09-771-287-12	Sequence 12, Appl1	C 623	10.4	47.3	25	9	US-10-098-263B-67859	Sequence 67859, A
C 551	10.4	47.3	22	10	US-09-797-858-2	Sequence 2, Appl1	C 624	10.4	47.3	25	9	US-10-098-263B-67859	Sequence 67859, A
C 552	10.4	47.3	22	10	US-09-797-858-2	Sequence 2, Appl1	C 625	10.4	47.3	25	9	US-10-098-263B-70148	Sequence 70148, A
C 553	10.4	47.3	23	9	US-09-816-814-19	Sequence 19, Appl1	C 626	10.4	47.3	25	9	US-10-098-263B-70148	Sequence 70148, A
C 554	10.4	47.3	23	9	US-09-816-814-19	Sequence 19, Appl1	C 627	10.4	47.3	25	9	US-10-098-263B-70774	Sequence 70774, A
C 555	10.4	47.3	24	7	US-08-964-716-30	Sequence 30, Appl1	C 628	10.4	47.3	25	9	US-10-098-263B-70774	Sequence 70774, A
C 556	10.4	47.3	24	7	US-08-964-716-30	Sequence 30, Appl1	C 629	10.4	47.3	25	9	US-10-098-263B-71735	Sequence 71735, A
C 557	10.4	47.3	24	9	US-09-888-326-806	Sequence 806, App	C 630	10.4	47.3	25	9	US-10-098-263B-71735	Sequence 71735, A
C 558	10.4	47.3	24	9	US-09-888-326-806	Sequence 806, App	C 631	10.4	47.3	25	9	US-10-098-263B-71735	Sequence 71735, A
C 559	10.4	47.3	24	9	US-10-112-653-808	Sequence 808, App	C 632	10.4	47.3	25	9	US-10-098-263B-74577	Sequence 74577, A
C 560	10.4	47.3	24	9	US-10-112-653-808	Sequence 808, App	C 633	10.4	47.3	25	9	US-10-098-263B-74577	Sequence 74577, A
C 561	10.4	47.3	24	9	US-10-017-995-837	Sequence 837, App	C 634	10.4	47.3	25	9	US-10-098-263B-82867	Sequence 82867, A
C 562	10.4	47.3	24	9	US-10-017-995-837	Sequence 837, App	C 635	10.4	47.3	25	9	US-10-098-263B-82867	Sequence 82867, A
C 563	10.4	47.3	24	9	US-09-776-479-837	Sequence 837, App	C 636	10.4	47.3	25	9	US-10-098-263B-88700	Sequence 88700, A
C 564	10.4	47.3	24	9	US-09-776-479-837	Sequence 837, App	C 637	10.4	47.3	25	9	US-10-098-263B-88700	Sequence 88700, A
C 565	10.4	47.3	24	9	US-09-940-185-3790	Sequence 3790, App	C 638	10.4	47.3	25	9	US-10-098-263B-92750	Sequence 92750, A
C 566	10.4	47.3	24	9	US-09-940-185-3790	Sequence 3790, App	C 639	10.4	47.3	25	9	US-10-098-263B-92750	Sequence 92750, A
C 567	10.4	47.3	25	9	US-09-990-659A-21	Sequence 21, Appl1	C 640	10.4	47.3	25	9	US-10-098-263B-94250	Sequence 94250, A
C 568	10.4	47.3	25	9	US-09-990-659A-21	Sequence 21, Appl1	C 641	10.4	47.3	25	9	US-10-098-263B-94250	Sequence 94250, A
C 569	10.4	47.3	25	9	US-10-215-112-4140	Sequence 4140, App	C 642	10.4	47.3	25	9	US-10-098-263B-95835	Sequence 95835, A
C 570	10.4	47.3	25	9	US-10-215-112-4140	Sequence 4140, App	C 643	10.4	47.3	25	9	US-10-098-263B-104176	Sequence 104176, A
C 571	10.4	47.3	25	9	US-10-215-112-5370	Sequence 5370, App	C 644	10.4	47.3	25	9	US-10-098-263B-104176	Sequence 104176, A
C 572	10.4	47.3	25	9	US-10-215-112-5370	Sequence 5370, App	C 645	10.4	47.3	25	9	US-10-098-263B-114336	Sequence 114336, A
C 573	10.4	47.3	25	9	US-10-215-112-12171	Sequence 12171, A	C 646	10.4	47.3	25	9	US-10-098-263B-114336	Sequence 114336, A
C 574	10.4	47.3	25	9	US-10-215-112-12171	Sequence 12171, A	C 647	10.4	47.3	25	9	US-10-098-263B-118959	Sequence 118959, A
C 575	10.4	47.3	25	9	US-10-215-112-12363	Sequence 12363, A	C 648	10.4	47.3	25	9	US-10-098-263B-118959	Sequence 118959, A
C 576	10.4	47.3	25	9	US-10-215-112-12363	Sequence 12363, A	C 649	10.4	47.3	25	9	US-10-098-263B-128186	Sequence 128186, A
C 577	10.4	47.3	25	9	US-10-215-112-13233	Sequence 13233, A	C 650	10.4	47.3	25	9	US-10-098-263B-128186	Sequence 128186, A
C 578	10.4	47.3	25	9	US-10-215-112-13233	Sequence 13233, A	C 651	10.4	47.3	25	9	US-10-098-263B-128186	Sequence 128186, A
C 579	10.4	47.3	25	9	US-10-098-263B-5730	Sequence 5730, App	C 652	10.4	47.3	25	9	US-10-098-263B-128692	Sequence 128692, A
C 580	10.4	47.3	25	9	US-10-098-263B-5730	Sequence 5730, App	C 653	10.4	47.3	25	9	US-10-098-263B-126041	Sequence 126041, A
C 581	10.4	47.3	25	9	US-10-098-263B-5773	Sequence 5773, App	C 654	10.4	47.3	25	9	US-10-098-263B-126041	Sequence 126041, A
C 582	10.4	47.3	25	9	US-10-098-263B-5773	Sequence 5773, App	C 655	10.4	47.3	25	9	US-10-098-263B-126319	Sequence 126319, A
C 583	10.4	47.3	25	9	US-10-098-263B-5774	Sequence 5774, App	C 656	10.4	47.3	25	9	US-10-098-263B-126319	Sequence 126319, A
C 584	10.4	47.3	25	9	US-10-098-263B-5774	Sequence 5774, App	C 657	10.4	47.3	25	9	US-10-098-263B-127920	Sequence 127920, A
C 585	10.4	47.3	25	9	US-10-098-263B-9754	Sequence 9754, App	C 658	10.4	47.3	25	9	US-10-098-263B-127920	Sequence 127920, A
C 586	10.4	47.3	25	9	US-10-098-263B-9754	Sequence 9754, App	C 659	10.4	47.3	25	9	US-10-098-263B-128868	Sequence 128868, A
C 587	10.4	47.3	25	9	US-10-098-263B-11517	Sequence 11517, A	C 660	10.4	47.3	25	9	US-10-098-263B-128868	Sequence 128868, A
C 588	10.4	47.3	25	9	US-10-098-263B-11517	Sequence 11517, A	C 661	10.4	47.3	25	10	US-09-887-576-535	Sequence 535, App
C 589	10.4	47.3	25	9	US-10-098-263B-11518	Sequence 11518, A	C 662	10.4	47.3	25	10	US-09-887-576-535	Sequence 535, App
C 590	10.4	47.3	25	9	US-10-098-263B-11518	Sequence 11518, A	C 663	10.4	47.3	25	9	US-09-844-517-12	Sequence 12, Appl1
C 591	10.4	47.3	25	9	US-10-098-263B-19164	Sequence 19164, A	C 664	10.4	47.3	25	9	US-09-844-517-12	Sequence 12, Appl1
C 592	10.4	47.3	25	9	US-10-098-263B-19164	Sequence 19164, A	C 665	10.4	47.3	25	9	US-10-195-752-18	Sequence 18, Appl1
C 593	10.4	47.3	25	9	US-10-098-263B-19164	Sequence 19164, A	C 666	10.4	47.3	25	9	US-10-195-752-18	Sequence 18, Appl1
C 594	10.4	47.3	25	9	US-10-098-263B-19768	Sequence 19768, A	C 667	10.4	47.3	25	9	US-10-265-713-6	Sequence 6, Appl1
C 595	10.4	47.3	25	9	US-10-098-263B-19768	Sequence 19768, A	C 668	10.4	47.3	25	9	US-10-265-713-6	Sequence 6, Appl1
C 596	10.4	47.3	25	9	US-10-098-263B-25136	Sequence 25136, A	C 669	10.4	47.3	25	9	US-09-764-304-6	Sequence 6, Appl1
C 597	10.4	47.3	25	9	US-10-098-263B-25136	Sequence 25136, A	C 670	10.4	47.3	25	10	US-09-764-304-6	Sequence 6, Appl1
C 598	10.4	47.3	25	9	US-10-098-263B-25444	Sequence 25444, A	C 671	10.4	47.3	25	10	US-09-772-120-1	Sequence 1, Appl1
C 599	10.4	47.3	25	9	US-10-098-263B-30335	Sequence 30335, A	C 672	10.4	47.3	25	10	US-09-772-120-1	Sequence 1, Appl1
C 600	10.4	47.3	25	9	US-10-098-263B-30335	Sequence 30335, A	C 673	10.4	47.3	25	10	US-09-753-436-31	Sequence 31, Appl1
C 601	10.4	47.3	25	9	US-10-098-263B-32765	Sequence 32765, A	C 674	10.4	47.3	25	10	US-09-753-436-31	Sequence 31, Appl1
C 602	10.4	47.3	25	9	US-10-098-263B-32765	Sequence 32765, A	C 675	10.4	47.3	25	10	US-09-253-794-41	Sequence 41, Appl1
C 603	10.4	47.3	25	9	US-10-098-263B-32766	Sequence 32766, A	C 676	10.4	47.3	25	10	US-09-253-794-41	Sequence 41, Appl1

C 677	10.4	47.3	31	10	US-09-910-059-2	Sequence 2, Appl1	C 750	10.4	47.3	48	9	US-09-907-575-357	Sequence 357, App
C 678	10.4	47.3	31	10	US-09-910-059-2	Sequence 2, Appl1	C 751	10.4	47.3	48	9	US-09-902-759-357	Sequence 357, App
C 679	10.4	47.3	33	9	US-10-189-576-16	Sequence 16, Appl	C 752	10.4	47.3	48	9	US-09-902-759-357	Sequence 357, App
C 680	10.4	47.3	33	9	US-10-189-576-16	Sequence 16, Appl	C 753	10.4	47.3	48	9	US-09-905-075-357	Sequence 357, App
C 681	10.4	47.3	33	10	US-09-912-962-21	Sequence 21, Appl	C 754	10.4	47.3	48	9	US-09-905-075-357	Sequence 357, App
C 682	10.4	47.3	33	10	US-09-912-962-21	Sequence 21, Appl	C 755	10.4	47.3	48	9	US-09-902-634-357	Sequence 357, App
C 683	10.4	47.3	38	9	US-09-844-517-17	Sequence 17, Appl	C 756	10.4	47.3	48	9	US-09-902-634-357	Sequence 357, App
C 684	10.4	47.3	38	9	US-09-844-517-17	Sequence 17, Appl	C 757	10.4	47.3	48	9	US-09-902-713-357	Sequence 357, App
C 685	10.4	47.3	48	9	US-09-905-291A-357	Sequence 357, App	C 758	10.4	47.3	48	9	US-09-902-713-357	Sequence 357, App
C 686	10.4	47.3	48	9	US-09-905-291A-357	Sequence 357, App	C 759	10.4	47.3	48	9	US-09-907-979-357	Sequence 357, App
C 687	10.4	47.3	48	9	US-09-902-853-357	Sequence 357, App	C 760	10.4	47.3	48	9	US-09-907-979-357	Sequence 357, App
C 688	10.4	47.3	48	9	US-09-902-853-357	Sequence 357, App	C 761	10.4	47.3	48	9	US-09-902-615-357	Sequence 357, App
C 689	10.4	47.3	48	9	US-09-907-824-357	Sequence 357, App	C 762	10.4	47.3	48	9	US-09-902-615-357	Sequence 357, App
C 690	10.4	47.3	48	9	US-09-907-824-357	Sequence 357, App	C 763	10.4	47.3	48	9	US-09-507-366-12	Sequence 12, Appl
C 691	10.4	47.3	48	9	US-09-907-841-357	Sequence 357, App	C 764	10.4	47.3	48	9	US-09-507-366-12	Sequence 12, Appl
C 692	10.4	47.3	48	9	US-09-907-841-357	Sequence 357, App	C 765	10.4	47.3	48	9	US-09-903-928-357	Sequence 357, App
C 693	10.4	47.3	48	9	US-09-904-011-357	Sequence 357, App	C 766	10.4	47.3	48	9	US-09-903-928-357	Sequence 357, App
C 694	10.4	47.3	48	9	US-09-904-011-357	Sequence 357, App	C 767	10.4	47.3	48	9	US-09-906-760A-357	Sequence 357, App
C 695	10.4	47.3	48	9	US-09-906-742-357	Sequence 357, App	C 768	10.4	47.3	48	9	US-09-906-760A-357	Sequence 357, App
C 696	10.4	47.3	48	9	US-09-906-742-357	Sequence 357, App	C 769	10.4	47.3	48	9	US-09-903-823-357	Sequence 357, App
C 697	10.4	47.3	48	9	US-09-906-838-357	Sequence 357, App	C 770	10.4	47.3	48	9	US-09-903-823-357	Sequence 357, App
C 698	10.4	47.3	48	9	US-09-906-838-357	Sequence 357, App	C 771	10.4	47.3	48	9	US-09-907-652-357	Sequence 357, App
C 699	10.4	47.3	48	9	US-09-907-613-357	Sequence 357, App	C 772	10.4	47.3	48	9	US-09-907-652-357	Sequence 357, App
C 700	10.4	47.3	48	9	US-09-907-613-357	Sequence 357, App	C 773	10.4	47.3	48	10	US-09-264-663A-20	Sequence 20, Appl
C 701	10.4	47.3	48	9	US-09-907-942-357	Sequence 357, App	C 774	10.4	47.3	48	10	US-09-264-663A-20	Sequence 20, Appl
C 702	10.4	47.3	48	9	US-09-907-942-357	Sequence 357, App	C 775	10.4	47.3	48	10	US-09-909-330-357	Sequence 357, App
C 703	10.4	47.3	48	9	US-09-907-942-357	Sequence 357, App	C 776	10.4	47.3	48	10	US-09-909-330-357	Sequence 357, App
C 704	10.4	47.3	48	9	US-09-904-820-357	Sequence 357, App	C 777	10.4	47.3	48	10	US-09-909-088B-357	Sequence 357, App
C 705	10.4	47.3	48	9	US-09-904-820-357	Sequence 357, App	C 778	10.4	47.3	48	10	US-09-909-088B-357	Sequence 357, App
C 706	10.4	47.3	48	9	US-09-904-859-357	Sequence 357, App	C 779	10.4	47.3	50	7	US-08-781-986A-3477	Sequence 3477, App
C 707	10.4	47.3	48	9	US-09-904-859-357	Sequence 357, App	C 780	10.4	47.3	50	7	US-08-781-986A-3477	Sequence 3477, App
C 708	10.4	47.3	48	9	US-09-909-204-357	Sequence 357, App	C 781	10.2	46.4	20	9	US-10-068-238-9	Sequence 9, Appl1
C 709	10.4	47.3	48	9	US-09-909-204-357	Sequence 357, App	C 782	10.2	46.4	20	9	US-10-068-238-9	Sequence 9, Appl1
C 710	10.4	47.3	48	9	US-09-904-786-357	Sequence 357, App	C 783	10.2	46.4	20	9	US-10-175-225-56	Sequence 56, Appl1
C 711	10.4	47.3	48	9	US-09-904-786-357	Sequence 357, App	C 784	10.2	46.4	20	9	US-10-175-225-56	Sequence 56, Appl1
C 712	10.4	47.3	48	9	US-09-906-646-357	Sequence 357, App	C 785	10.2	46.4	22	9	US-10-112-653-929	Sequence 929, App
C 713	10.4	47.3	48	9	US-09-906-646-357	Sequence 357, App	C 786	10.2	46.4	22	9	US-10-112-653-929	Sequence 929, App
C 714	10.4	47.3	48	9	US-09-906-700-357	Sequence 357, App	C 787	10.2	46.4	22	9	US-10-017-995-975	Sequence 975, App
C 715	10.4	47.3	48	9	US-09-906-700-357	Sequence 357, App	C 788	10.2	46.4	22	9	US-10-017-995-975	Sequence 975, App
C 716	10.4	47.3	48	9	US-09-902-903-357	Sequence 357, App	C 789	10.2	46.4	22	9	US-10-017-995-1045	Sequence 1045, App
C 717	10.4	47.3	48	9	US-09-902-903-357	Sequence 357, App	C 790	10.2	46.4	22	9	US-10-017-995-1045	Sequence 1045, App
C 718	10.4	47.3	48	9	US-09-903-749A-357	Sequence 357, App	C 791	10.2	46.4	22	9	US-09-776-479-975	Sequence 975, App
C 719	10.4	47.3	48	9	US-09-903-749A-357	Sequence 357, App	C 792	10.2	46.4	22	9	US-09-776-479-975	Sequence 975, App
C 720	10.4	47.3	48	9	US-09-903-786-357	Sequence 357, App	C 793	10.2	46.4	22	9	US-09-776-479-1045	Sequence 1045, App
C 721	10.4	47.3	48	9	US-09-902-713-357	Sequence 357, App	C 794	10.2	46.4	22	9	US-09-776-479-1045	Sequence 1045, App
C 722	10.4	47.3	48	9	US-09-902-713-357	Sequence 357, App	C 795	10.2	46.4	25	9	US-10-215-112-959	Sequence 959, App
C 723	10.4	47.3	48	9	US-09-904-119-357	Sequence 357, App	C 796	10.2	46.4	25	9	US-10-215-112-959	Sequence 959, App
C 724	10.4	47.3	48	9	US-09-904-119-357	Sequence 357, App	C 797	10.2	46.4	25	9	US-10-215-112-7222	Sequence 7222, App
C 725	10.4	47.3	48	9	US-09-904-956-357	Sequence 357, App	C 798	10.2	46.4	25	9	US-10-215-112-7222	Sequence 7222, App
C 726	10.4	47.3	48	9	US-09-904-956-357	Sequence 357, App	C 799	10.2	46.4	25	9	US-10-215-112-9395	Sequence 9395, App
C 727	10.4	47.3	48	9	US-09-907-794-357	Sequence 357, App	C 800	10.2	46.4	25	9	US-10-215-112-9395	Sequence 9395, App
C 728	10.4	47.3	48	9	US-09-907-794-357	Sequence 357, App	C 801	10.2	46.4	25	9	US-10-098-263B-371	Sequence 371, App
C 729	10.4	47.3	48	9	US-09-902-692-357	Sequence 357, App	C 802	10.2	46.4	25	9	US-10-098-263B-371	Sequence 371, App
C 730	10.4	47.3	48	9	US-09-902-692-357	Sequence 357, App	C 803	10.2	46.4	25	9	US-10-098-263B-372	Sequence 372, App
C 731	10.4	47.3	48	9	US-09-903-520-357	Sequence 357, App	C 804	10.2	46.4	25	9	US-10-098-263B-472	Sequence 472, App
C 732	10.4	47.3	48	9	US-09-903-520-357	Sequence 357, App	C 805	10.2	46.4	25	9	US-10-098-263B-1485	Sequence 1485, App
C 733	10.4	47.3	48	9	US-09-903-943-357	Sequence 357, App	C 806	10.2	46.4	25	9	US-10-098-263B-1485	Sequence 1485, App
C 734	10.4	47.3	48	9	US-09-903-943-357	Sequence 357, App	C 807	10.2	46.4	25	9	US-10-098-263B-1108	Sequence 1108, App
C 735	10.4	47.3	48	9	US-09-904-462-357	Sequence 357, App	C 808	10.2	46.4	25	9	US-10-098-263B-1108	Sequence 1108, App
C 736	10.4	47.3	48	9	US-09-904-462-357	Sequence 357, App	C 809	10.2	46.4	25	9	US-10-098-263B-4604	Sequence 4604, App
C 737	10.4	47.3	48	9	US-09-905-056-357	Sequence 357, App	C 810	10.2	46.4	25	9	US-10-098-263B-4604	Sequence 4604, App
C 738	10.4	47.3	48	9	US-09-905-056-357	Sequence 357, App	C 811	10.2	46.4	25	9	US-10-098-263B-4804	Sequence 4804, App
C 739	10.4	47.3	48	9	US-09-907-925-357	Sequence 357, App	C 812	10.2	46.4	25	9	US-10-098-263B-4804	Sequence 4804, App
C 740	10.4	47.3	48	9	US-09-907-925-357	Sequence 357, App	C 813	10.2	46.4	25	9	US-10-098-263B-5667	Sequence 5667, App
C 741	10.4	47.3	48	9	US-09-904-553-357	Sequence 357, App	C 814	10.2	46.4	25	9	US-10-098-263B-5667	Sequence 5667, App
C 742	10.4	47.3	48	9	US-09-904-553-357	Sequence 357, App	C 815	10.2	46.4	25	9	US-10-098-263B-7308	Sequence 7308, App
C 743	10.4	47.3	48	9	US-09-905-381-357	Sequence 357, App	C 816	10.2	46.4	25	9	US-10-098-263B-7308	Sequence 7308, App
C 744	10.4	47.3	48	9	US-09-905-381-357	Sequence 357, App	C 817	10.2	46.4	25	9	US-10-098-263B-7396	Sequence 7396, App
C 745	10.4	47.3	48	9	US-09-909-064-357	Sequence 357, App	C 818	10.2	46.4	25	9	US-10-098-263B-7396	Sequence 7396, App
C 746	10.4	47.3	48	9	US-09-909-064-357	Sequence 357, App	C 819	10.2	46.4	25	9	US-10-098-263B-8321	Sequence 8321, App
C 747	10.4	47.3	48	9	US-09-905-088-357	Sequence 357, App	C 820	10.2	46.4	25	9	US-10-098-263B-8321	Sequence 8321, App
C 748	10.4	47.3	48	9	US-09-905-088-357	Sequence 357, App	C 821	10.2	46.4	25	9	US-10-098-263B-13102	Sequence 13102, A
C 749	10.4	47.3	48	9	US-09-907-575-357	Sequence 357, App	C 822	10.2	46.4	25	9	US-10-098-263B-13102	Sequence 13102, A


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c 973 10 45.5 25 9 US-09-754-853A-697 Sequence 697, App
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c 994 10 45.5 25 9 US-10-098-263B-3530 Sequence 3530, Ap
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c 996 10 45.5 25 9 US-10-098-263B-5439 Sequence 5439, Ap
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ALIGNMENTS

RESULT 1

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; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 30445
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-30445
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Db 3 CTTCTACCGATATTTGCTCAG 24
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; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
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; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 30445
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-30445
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Best Local Similarity 77.3%; Pred. No. 7.9e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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Db 24 CTTCTACCGATATTTGCTCAG 3
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RESULT 3

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; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 70455
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-70455
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Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 4

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US-10-098-263B-70455/c
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; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 70455
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-70455
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Query Match 63.6%; Score 14; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGAGACCGATATC 14
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Db 18 CTGAGACCGATATC 5

RESULT 5

US-10-098-263B-87625
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; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; PRIOR FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 87625
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-87625

Query Match 63.6%; Score 14; DB 9; Length 25;
Best Local Similarity 77.3%; Pred. No. 7.9e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CTGAGACCGATATCGTCTCAG 22
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Db 2 CTGATACCAATATGAGTCTCG 23

RESULT 6

US-10-098-263B-87625/c
; Sequence 87625, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; PRIOR FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 87625
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-87625

Query Match 63.6%; Score 14; DB 9; Length 25;
Best Local Similarity 77.3%; Pred. No. 7.9e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CTGAGACCGATATCGTCTCAG 22
| | | | | | | | | | | | | | | |
Db 23 CGGAGACTCATATGCTATCAG 2

RESULT 7

US-10-098-263B-105385
; Sequence 105385, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1

; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 105385
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-105385

Query Match 63.6%; Score 14; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GATATCGGTCTCAG 22
| | | | | | | | | | | | | | | |
Db 1 GATATCGGTCTCAG 14

RESULT 8

US-10-098-263B-105385/c
; Sequence 105385, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; PRIOR FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 105385
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-105385

Query Match 63.6%; Score 14; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGAGACCGATATC 14
| | | | | | | | | | | | | | | |
Db 14 CTGAGACCGATATC 1

RESULT 9

US-10-098-263B-67902
; Sequence 67902, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; PRIOR FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 67902
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-67902

Query Match 61.8%; Score 13.6; DB 9; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.3e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 CTGAGACCGATATCGTCTC 20
Db 4 CGGACGACGATTTCCGTCCG 23

RESULT 10

US-10-098-263B-67902/c
; Sequence 67902, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO: 67902
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-67902

Query Match 61.8%; Score 13.6; DB 9; Length 25;
Beat Local Similarity 80.0%; Pred. No. 1.3e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 3 GAGACCGATATCGTCTCAG 22
Db 23 GCGACGACGATTTCTCTCCG 4

RESULT 11

US-10-098-263B-93368
; Sequence 93368, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO: 93368
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-93368

Query Match 61.8%; Score 13.6; DB 9; Length 25;
Beat Local Similarity 80.0%; Pred. No. 1.3e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 CTGAGACCGATATCGTCTC 20
Db 2 CGGACGACGATTTCCGTCCG 21

RESULT 12

US-10-098-263B-93368/c
; Sequence 93368, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B

; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO: 93368
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-93368

Query Match 61.8%; Score 13.6; DB 9; Length 25;
Beat Local Similarity 80.0%; Pred. No. 1.3e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 3 GAGACCGATATCGTCTCAG 22
Db 21 GCGACGACGATTTCTCTCCG 2

RESULT 13

US-10-098-263B-42695
; Sequence 42695, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO: 42695
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-42695

Query Match 60.0%; Score 13.2; DB 9; Length 25;
Beat Local Similarity 83.3%; Pred. No. 2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 5 GACCGATATCGTCTCAG 22
Db 1 GACGACATCGTCTCTG 18

RESULT 14

US-10-098-263B-42695/c
; Sequence 42695, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO: 42695
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-42695

Query Match 60.0%; Score 13.2; DB 9; Length 25;
Beat Local Similarity 83.3%; Pred. No. 2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 CTGAGACCGATATCGGTC 18
Db 18 CAGAGACCGATATCGGTC 1

RESULT 15
US-10-098-263B-83125

; Sequence 83125, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:

; APPLICANT: Mitteran, Michael

; TITLE OF INVENTION: Human Microarray

; FILE REFERENCE: 3118.1

; CURRENT APPLICATION NUMBER: US/10/098,263B

; PRIOR FILING DATE: 2003-01-08

; PRIORITY APPLICATION NUMBER: 60/276,759

; NUMBER OF SEQ ID NOS: 131066

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 83125

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Homo sapien

US-10-098-263B-83125

Query Match 59.1%; Score 13; DB 9; Length 25;
Best Local Similarity 76.2%; Pred. No. 2.6e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 2 TGAGACCGATATCGGTCGAG 22
Db 3 TGACACCCCTATAGGTCCTCCG 23

RESULT 16

US-10-098-263B-83125/c

; Sequence 83125, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:

; APPLICANT: Mitteran, Michael

; TITLE OF INVENTION: Human Microarray

; FILE REFERENCE: 3118.1

; CURRENT APPLICATION NUMBER: US/10/098,263B

; PRIOR FILING DATE: 2003-01-08

; PRIORITY APPLICATION NUMBER: 60/276,759

; NUMBER OF SEQ ID NOS: 131066

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 83125

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Homo sapien

US-10-098-263B-83125

Query Match 59.1%; Score 13; DB 9; Length 25;
Best Local Similarity 76.2%; Pred. No. 2.6e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 CTGAGACCGATATCGGTCCTCA 21
Db 23 CGGAGACCTATAGGGGTCTCA 3

RESULT 17

US-10-011-931-41

; Sequence 41, Application US/10011931
; Publication No. US20030026806A1
; GENERAL INFORMATION:

; APPLICANT: WITTE, ALISON

; APPLICANT: VANUM, BRIAN C.

; APPLICANT: QIAN, ZUEMING

; APPLICANT: VEZINA, CHRIS

; TITLE OF INVENTION: ANTIBODIES AND OTHER SELECTIVE IL-1 BINDING AGENTS THAT ALLOW BINDING

; TITLE OF INVENTION: IL-1 RECEPTOR BUT NOT ACTIVATION THEREOF
; FILE REFERENCE: A-731
; CURRENT APPLICATION NUMBER: US/10/011,931
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: US 60/244,118
; PRIOR FILING DATE: 2000-10-27
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 41
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: KAPPA CHAIN HUMANIZATION OLIGONUCLEOTIDE
US-10-011-931-41

Query Match 59.1%; Score 13; DB 9; Length 33;
Best Local Similarity 76.2%; Pred. No. 2.6e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 2 TGAGACCGATATCGGTCGAG 22
Db 3 TGAGAGTGAAGTCGTCCTCCG 23

RESULT 18

US-10-011-931-41/c

; Sequence 41, Application US/10011931
; Publication No. US20030026806A1
; GENERAL INFORMATION:

; APPLICANT: WITTE, ALISON

; APPLICANT: VANUM, BRIAN C.

; APPLICANT: QIAN, ZUEMING

; APPLICANT: VEZINA, CHRIS

; TITLE OF INVENTION: ANTIBODIES AND OTHER SELECTIVE IL-1 BINDING AGENTS THAT ALLOW BINDING

; FILE REFERENCE: A-731
; CURRENT APPLICATION NUMBER: US/10/011,931
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: US 60/244,118
; PRIOR FILING DATE: 2000-10-27
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 41
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: KAPPA CHAIN HUMANIZATION OLIGONUCLEOTIDE
US-10-011-931-41

Query Match 59.1%; Score 13; DB 9; Length 33;
Best Local Similarity 76.2%; Pred. No. 2.6e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 CTGAGACCGATATCGGTCCTCA 21
Db 23 CTGGGACCGACTTACTCTCA 3

RESULT 19

US-10-011-931-42

; Sequence 42, Application US/10011931
; Publication No. US20030026806A1
; GENERAL INFORMATION:

; APPLICANT: WITTE, ALISON

; APPLICANT: VANUM, BRIAN C.

; APPLICANT: QIAN, ZUEMING

; APPLICANT: VEZINA, CHRIS

; TITLE OF INVENTION: ANTIBODIES AND OTHER SELECTIVE IL-1 BINDING AGENTS THAT ALLOW BINDING

; FILE REFERENCE: A-731
; CURRENT APPLICATION NUMBER: US/10/011,931

```

; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: US 60/244,118
; PRIOR FILING DATE: 2000-10-27
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: KAPPA CHAIN HUMANIZATION OLIGONUCLEOTIDE
US-10-011-931-42

Query Match          59.1%; Score 13; DB 9; Length 33;
Best Local Similarity 76.2%; Pred. No. 2.6e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy      1 CTGAGACCGATATCGGTCTCA 21
        ||| ||| ||| ||| ||| |||
Db      8 CTGGAGCCGACTTCACTCTCA 28

RESULT 20
US-10-011-931-42/c
; Sequence 42, Application US/10011931
; Publication No. US20030026806A1
; GENERAL INFORMATION:
; APPLICANT: WITTE, ALISON
; APPLICANT: VARNUM, BRIAN C.
; APPLICANT: QIAN, ZUEMING
; APPLICANT: VEZINA, CHRIS
; TITLE OF INVENTION: ANTIBODIES AND OTHER SELECTIVE IL-1 BINDING AGENTS THAT ALLOW BIN
; TITLE OF INVENTION: IL-1 RECEPTOR BUT NOT ACTIVATION THEREOF
; FILE REFERENCE: A-731
; CURRENT APPLICATION NUMBER: US/10/011,931
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: US 60/244,118
; PRIOR FILING DATE: 2000-10-27
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: KAPPA CHAIN HUMANIZATION OLIGONUCLEOTIDE
US-10-011-931-42

Query Match          59.1%; Score 13; DB 9; Length 33;
Best Local Similarity 76.2%; Pred. No. 2.6e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy      2 TGAGACCGATATCGGTCTCAG 22
        ||| ||| ||| ||| ||| |||
Db      28 TGAGAGTGAGTGGTCCAG 8

RESULT 21
US-10-011-931-56
; Sequence 56, Application US/10011931
; Publication No. US20030026806A1
; GENERAL INFORMATION:
; APPLICANT: WITTE, ALISON
; APPLICANT: VARNUM, BRIAN C.
; APPLICANT: QIAN, ZUEMING
; APPLICANT: VEZINA, CHRIS
; TITLE OF INVENTION: ANTIBODIES AND OTHER SELECTIVE IL-1 BINDING AGENTS THAT ALLOW BIN
; TITLE OF INVENTION: IL-1 RECEPTOR BUT NOT ACTIVATION THEREOF
; FILE REFERENCE: A-731
; CURRENT APPLICATION NUMBER: US/10/011,931
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: US 60/244,118
; PRIOR FILING DATE: 2000-10-27
; SEQ ID NO 57
```

```

; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 56
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: KAPPA CHAIN HUMANIZATION OLIGONUCLEOTIDE
US-10-011-931-56

Query Match          59.1%; Score 13; DB 9; Length 33;
Best Local Similarity 76.2%; Pred. No. 2.6e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy      2 TGAGACCGATATCGGTCTCAG 22
        ||| ||| ||| ||| ||| |||
Db      3 TGAGAGTGAGTGGTCCAG 23

RESULT 22
US-10-011-931-56/c
; Sequence 56, Application US/10011931
; Publication No. US20030026806A1
; GENERAL INFORMATION:
; APPLICANT: WITTE, ALISON
; APPLICANT: VARNUM, BRIAN C.
; APPLICANT: QIAN, ZUEMING
; APPLICANT: VEZINA, CHRIS
; TITLE OF INVENTION: ANTIBODIES AND OTHER SELECTIVE IL-1 BINDING AGENTS THAT ALLOW BI
; TITLE OF INVENTION: IL-1 RECEPTOR BUT NOT ACTIVATION THEREOF
; FILE REFERENCE: A-731
; CURRENT APPLICATION NUMBER: US/10/011,931
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: US 60/244,118
; PRIOR FILING DATE: 2000-10-27
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 56
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: KAPPA CHAIN HUMANIZATION OLIGONUCLEOTIDE
US-10-011-931-56

Query Match          59.1%; Score 13; DB 9; Length 33;
Best Local Similarity 76.2%; Pred. No. 2.6e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy      1 CTGAGACCGATATCGGTCTCA 21
        ||| ||| ||| ||| ||| |||
Db      23 CTGGAGCCGACTTCACTCTCA 3

RESULT 23
US-10-011-931-57
; Sequence 57, Application US/10011931
; Publication No. US20030026806A1
; GENERAL INFORMATION:
; APPLICANT: WITTE, ALISON
; APPLICANT: VARNUM, BRIAN C.
; APPLICANT: QIAN, ZUEMING
; APPLICANT: VEZINA, CHRIS
; TITLE OF INVENTION: ANTIBODIES AND OTHER SELECTIVE IL-1 BINDING AGENTS THAT ALLOW BI
; TITLE OF INVENTION: IL-1 RECEPTOR BUT NOT ACTIVATION THEREOF
; FILE REFERENCE: A-731
; CURRENT APPLICATION NUMBER: US/10/011,931
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: US 60/244,118
; PRIOR FILING DATE: 2000-10-27
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57
```


LENGTH: 33
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: KAPPA CHAIN HUMANIZATION OLIGONUCLEOTIDE
US-10-011-931-57

Query Match 59.1%; Score 13; DB 9; Length 33;
Best Local Similarity 76.2%; Pred. No. 2.6e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 1 CTGAGACCGATATCGGTCTCA 21
Db 8 CTGGGACCGACTTCACTCTCA 28

RESULT 24
US-10-011-931-57/c
Sequence 57, Application US/10011931
Publication No. US20030026806A1
GENERAL INFORMATION:
APPLICANT: WITTE, ALISON
APPLICANT: VANUM, BRIAN C.
APPLICANT: QIAN, ZUENING
APPLICANT: VEZINA, CHRIS
TITLE OF INVENTION: ANTIBODIES AND OTHER SELECTIVE IL-1 BINDING AGENTS THAT ALLOW BIN
TITLE OF INVENTION: IL-1 RECEPTOR BUT NOT ACTIVATION THEREOF
FILE REFERENCE: A-731
CURRENT APPLICATION NUMBER: US/10/011,931
CURRENT FILING DATE: 2002-04-01
PRIOR APPLICATION NUMBER: US 60/244,118
PRIOR FILING DATE: 2000-10-27
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PatentIn version 3.1
SEQ ID NO 57
LENGTH: 33
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: KAPPA CHAIN HUMANIZATION OLIGONUCLEOTIDE
US-10-011-931-57

Query Match 59.1%; Score 13; DB 9; Length 33;
Best Local Similarity 76.2%; Pred. No. 2.6e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 2 TGAGACCGATATCGGTCTCAG 22
Db 28 TGAGAGTGAAGTCGTCCTCCAG 8

RESULT 25
US-10-098-263B-60005
Sequence 60005, Application US/10098263B
Publication No. US20030104410A1
GENERAL INFORMATION:
APPLICANT: Miltman, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: 60/276,759
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 60005
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-10-098-263B-60005

Query Match 58.2%; Score 12.8; DB 9; Length 25;
Best Local Similarity 87.5%; Pred. No. 3.2e+03;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 6 ACCGATATCGGTCTCA 21
Db 5 ACCGACATCGATCTCA 20

RESULT 26
US-10-098-263B-60005/c
Sequence 60005, Application US/10098263B
Publication No. US20030104410A1
GENERAL INFORMATION:
APPLICANT: Miltman, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: 60/276,759
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 60005
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-10-098-263B-60005

Query Match 58.2%; Score 12.8; DB 9; Length 25;
Best Local Similarity 87.5%; Pred. No. 3.2e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 TGAGACCGATATCGGT 17
Db 20 TGAGATCATGTCTGT 5

RESULT 27
US-10-098-263B-88139
Sequence 88139, Application US/10098263B
Publication No. US20030104410A1
GENERAL INFORMATION:
APPLICANT: Miltman, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: 60/276,759
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 88139
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-10-098-263B-88139

Query Match 58.2%; Score 12.8; DB 9; Length 25;
Best Local Similarity 87.5%; Pred. No. 3.2e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 5 GACCGATATCGGTCTC 20
Db 7 GACCCGATATCGGTCTC 22

RESULT 28
US-10-098-263B-88139/c
Sequence 88139, Application US/10098263B
Publication No. US20030104410A1
GENERAL INFORMATION:
APPLICANT: Miltman, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1

```
;; CURRENT APPLICATION NUMBER: US/10/098,263B
;; CURRENT FILING DATE: 2003-01-08
;; PRIOR APPLICATION NUMBER: 60/276,759
;; PRIOR FILING DATE: 2001-03-16
;; NUMBER OF SEQ ID NOS: 131066
;; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
;; SEQ ID NO 88139
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: Homo sapien
US-10-098-263B-88139

Query Match          58.2%; Score 12.6; DB 9; Length 25;
Best Local Similarity 87.5%; Pred. No. 3.2e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAGACCGATATCGGTC 18
Db 22 GAGACCGATATCGGTC 7

RESULT 29
US-09-745-317-15
; Sequence 15, Application US/09745317
; Publication No. US20020187470A1
; GENERAL INFORMATION:
; APPLICANT: Casey, Warren
; APPLICANT: Chen, Jingwen
; APPLICANT: Much, Heidi
; APPLICANT: Taylor, David
; APPLICANT: Weiner, Michael Philip
; TITLE OF INVENTION: DETECTION OF SINGLE NUCLEOTIDE
; TITLE OF INVENTION: POLYMORPHISMS
; FILE REFERENCE: 07083,000602
; CURRENT APPLICATION NUMBER: US/09/745,317
; CURRENT FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/173,268
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/No. US20020187470A1e =
US-09-745-317-15

Query Match          57.3%; Score 12.6; DB 9; Length 25;
Best Local Similarity 78.9%; Pred. No. 4.1e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 GAGACCGATATCGGTC 21
Db 5 GATACCGATCTCGGCCCA 23

RESULT 30
US-09-745-317-15/c
; Sequence 15, Application US/09745317
; Publication No. US20020187470A1
; GENERAL INFORMATION:
; APPLICANT: Casey, Warren
; APPLICANT: Chen, Jingwen
; APPLICANT: Much, Heidi
; APPLICANT: Taylor, David
; APPLICANT: Weiner, Michael Philip
; TITLE OF INVENTION: DETECTION OF SINGLE NUCLEOTIDE
; TITLE OF INVENTION: POLYMORPHISMS
; FILE REFERENCE: 07083,000602
; CURRENT APPLICATION NUMBER: US/09/745,317
; CURRENT FILING DATE: 2000-12-21
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;; PRIOR APPLICATION NUMBER: 60/173,268
;; PRIOR FILING DATE:
;; NUMBER OF SEQ ID NOS: 112
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 15
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/No. US20020187470A1e =
US-09-745-317-15

Query Match          57.3%; Score 12.6; DB 9; Length 25;
Best Local Similarity 78.9%; Pred. No. 4.1e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 TGAGACCGATATCGGTC 20
Db 23 TGCGCCGAGATCGGTATC 5

RESULT 31
US-10-098-263B-130373
; Sequence 130373, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 130373
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-130373

Query Match          57.3%; Score 12.6; DB 9; Length 25;
Best Local Similarity 78.9%; Pred. No. 4.1e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 GAGACCGATATCGGTC 21
Db 4 GAAACGATATCGGTATCA 22

RESULT 32
US-10-098-263B-130373/c
; Sequence 130373, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 130373
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-130373

Query Match          57.3%; Score 12.6; DB 9; Length 25;
Best Local Similarity 78.9%; Pred. No. 4.1e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2 TGAGACCGATATCGTCTC 20
Db 22 TGATACCGATATCGTTTC 4

RESULT 33

US-10-098-263B-21859
; Sequence 21859, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; PRIOR FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 21859
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-21859

Query Match 56.4%; Score 12.4; DB 9; Length 25;
Best Local Similarity 92.9%; Pred. No. 5.2e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CGATATCGTCTCA 21
Db 11 CGATATCGTCTCCA 24

RESULT 34

US-10-098-263B-21859/c
; Sequence 21859, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; PRIOR FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 21859
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-21859

Query Match 56.4%; Score 12.4; DB 9; Length 25;
Best Local Similarity 92.9%; Pred. No. 5.2e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGAGACCGATATCG 15
Db 24 TGGAGCCGATATCG 11

RESULT 35

US-10-098-263B-30446
; Sequence 30446, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1

; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2003-01-08
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 30446
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-30446

Query Match 56.4%; Score 12.4; DB 9; Length 25;
Best Local Similarity 72.7%; Pred. No. 5.2e+03;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CTGAGACCGATATCGTCTCAG 22
Db 3 CTCTACCGAATTTGCTCAG 24

RESULT 36

US-10-098-263B-30446/c
; Sequence 30446, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; PRIOR FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 30446
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-30446

Query Match 56.4%; Score 12.4; DB 9; Length 25;
Best Local Similarity 72.7%; Pred. No. 5.2e+03;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CTGAGACCGATATCGTCTCAG 22
Db 24 CTGAGACCAATTTGCTAGAAG 3

RESULT 37

US-10-098-263B-70456
; Sequence 70456, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; PRIOR FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 70456
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-70456

Query Match 56.4%; Score 12.4; DB 9; Length 25;
Best Local Similarity 92.9%; Pred. No. 5.2e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 9 GATATCGGCTCAG 22
|||||
Db 5 GATATCGGCTCAG 18

RESULT 38
US-10-098-263B-70456/c
; Sequence 70456, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 70456
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-70456

Query Match 56.4%; Score 12.4; DB 9; Length 25;
Best Local Similarity 92.9%; Pred. No. 5.2e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CTGAGACCGATATC 14
|||||
Db 18 CTGAGTCGATATC 5

RESULT 39
US-10-098-263B-87626
; Sequence 87626, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 87626
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-87626

Query Match 56.4%; Score 12.4; DB 9; Length 25;
Best Local Similarity 72.7%; Pred. No. 5.2e+03;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 CTGAGACCGATATCGGCTCAG 22
|||||
Db 2 CTGATACCAATTGTGAGTCTCG 23

RESULT 40
US-10-098-263B-87626/c
; Sequence 87626, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B

; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 87626
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-87626

Query Match 56.4%; Score 12.4; DB 9; Length 25;
Best Local Similarity 72.7%; Pred. No. 5.2e+03;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 CTGAGACCGATATCGGCTCAG 22
|||||
Db 23 CGGAGCTCAATTGTGATCAG 2

Search completed: June 14, 2003, 23:29:10
Job time : 125 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 14, 2003, 19:02:55 ; Search time 1368 Seconds

(Without alignments)
260.454 Million cell updates/sec

Title: US-09-532-001-1

Perfect score: 22 CTGAGACCGATATCGTCTCAG 22

Sequence: 1 CTGAGACCGATATCGTCTCAG 22

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

EST:*
1: em_estba:*
2: em_esthna:*
3: em_estln:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estrom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_hiv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12.6	57.3	48	9	A1749566 ac30f01.x
2	12.6	57.3	48	9	A1749566 ac30f01.x
3	12.4	56.4	50	9	AUI03408 AUI03408
4	12.4	56.4	50	9	AUI03408 AUI03408
5	12	54.5	32	17	AZ511046 AUI035120
6	12	54.5	32	17	AZ511046 IM0355120

7	12	54.5	37	14	N32567	N32567 yw86e05.s1
8	12	54.5	37	14	N32567	N32567 yw86e05.s1
9	12	54.5	39	13	B1769009	B1769009 603058167
10	12	54.5	39	13	B1769009	B1769009 603058167
11	12	54.5	50	9	AUI06749	AUI06749 AUI06749
12	12	54.5	50	9	AUI06749	AUI06749 AUI06749
13	12	54.5	50	9	AUI07183	AUI07183 AUI07183
14	12	54.5	50	9	AUI07183	AUI07183 AUI07183
15	12	54.5	50	9	AUI07184	AUI07184 AUI07184
16	12	54.5	50	9	AUI07184	AUI07184 AUI07184
17	12	54.5	50	9	AUI07185	AUI07185 AUI07185
18	12	54.5	50	9	AUI07185	AUI07185 AUI07185
19	12	54.5	50	9	AUI07188	AUI07188 AUI07188
20	12	54.5	50	9	AUI07188	AUI07188 AUI07188
21	12	54.5	50	9	AUI07189	AUI07189 AUI07189
22	12	54.5	50	9	AUI07189	AUI07189 AUI07189
23	11.8	53.6	32	9	AUI03431	AUI03431 AUI03431
24	11.8	53.6	32	9	AUI03431	AUI03431 AUI03431
25	11.8	53.6	42	17	BH805089	BH805089 100806500
26	11.8	53.6	42	17	BH805089	BH805089 100806500
27	11.8	53.6	43	17	AZ304932	AZ304932 1M0005G03
28	11.8	53.6	43	17	AZ304932	AZ304932 1M0005G03
29	11.6	52.7	48	9	AUI03871	AUI03871 oc46c06.s
30	11.6	52.7	48	9	AUI03871	AUI03871 oc46c06.s
31	11.6	52.7	50	9	AUI07186	AUI07186 AUI07186
32	11.6	52.7	50	9	AUI07186	AUI07186 AUI07186
33	11.4	51.8	32	9	AUI03455	AUI03455 AUI03455
34	11.4	51.8	32	9	AUI03455	AUI03455 AUI03455
35	11.4	51.8	34	9	AUI03784	AUI03784 AUI03784
36	11.4	51.8	34	9	AUI03784	AUI03784 AUI03784
37	11.4	51.8	34	9	AUI03851	AUI03851 AUI03851
38	11.4	51.8	34	9	AUI03851	AUI03851 AUI03851
39	11.4	51.8	38	10	AV833036	AV833036 AV833036
40	11.4	51.8	38	10	AV833036	AV833036 AV833036
41	11.4	51.8	46	9	AUI06689	AUI06689 AUI06689
42	11.4	51.8	46	9	AUI06689	AUI06689 AUI06689
43	11.4	51.8	46	17	BH863926	BH863926 SALK_0949
44	11.4	51.8	46	17	BH863926	BH863926 SALK_0949
45	11.4	51.8	49	10	AW169662	AW169662 xj30606.x
46	11.4	51.8	49	10	AW169662	AW169662 xj30606.x
47	11.4	51.8	50	9	AUI04209	AUI04209 AUI04209
48	11.4	51.8	50	9	AUI04209	AUI04209 AUI04209
49	11.2	50.9	35	17	AZ591883	AZ591883 1M0402114
50	11.2	50.9	35	17	AZ591883	AZ591883 1M0402114
51	11.2	50.9	50	9	AUI07997	AUI07997 AUI07997
52	11.2	50.9	50	9	AUI07997	AUI07997 AUI07997
53	11.2	50.9	37	17	AZ806455	AZ806455 2M0068E04
54	11.2	50.9	37	17	AZ806455	AZ806455 2M0068E04
55	11.2	50.9	45	17	AZ810468	AZ810468 2M0076E02
56	11.2	50.9	45	17	AZ810468	AZ810468 2M0076E02
57	11.2	50.9	47	9	AUI258690	AUI258690 AUI258690
58	11.2	50.9	47	9	AUI258690	AUI258690 AUI258690
59	11.2	50.9	48	13	BM285362	BM285362 EST00003
60	11.2	50.9	48	13	BM285362	BM285362 EST00003
61	11.2	50.9	48	13	BM493234	BM493234 EST00017
62	11.2	50.9	48	13	BM493234	BM493234 EST00017
63	11.2	50.9	48	14	BO094078	BO094078 040802_37
64	11.2	50.9	48	14	BO094078	BO094078 040802_37
65	11.2	50.9	48	14	BO094080	BO094080 040802_39
66	11.2	50.9	48	14	BO094080	BO094080 040802_39
67	11.2	50.9	48	14	BO094081	BO094081 040802_40
68	11.2	50.9	48	14	BO094081	BO094081 040802_40
69	11.2	50.9	48	14	BO094082	BO094082 040802_41
70	11.2	50.9	48	14	BO094082	BO094082 040802_41
71	11.2	50.9	48	14	BO094086	BO094086 040802_45
72	11.2	50.9	48	14	BO094086	BO094086 040802_45
73	11.2	50.9	48	14	BO094088	BO094088 040802_47
74	11.2	50.9	48	14	BO094088	BO094088 040802_47
75	11.2	50.9	50	9	AUI03727	AUI03727 AUI03727
76	11.2	50.9	50	9	AUI03727	AUI03727 AUI03727
77	10.8	49.1	28	10	AW248289	AW248289 2819864.5
78	10.8	49.1	28	10	AW248289	AW248289 2819864.5
79	10.8	49.1	40	9	AUI880105	AUI880105 ap31d02.x

C 80	10.8	49.1	40	9	AI180105	AI180105	apj1d02.x	153	10	45.5	43	17	AZ830602	AZ830602	2M0109N24
C 81	10.8	49.1	40	17	AZ645161	AZ645161	IM0510N19	C 154	10	45.5	43	17	AZ830602	AZ830602	2M0109N24
C 82	10.8	49.1	40	17	AZ645161	AZ645161	IM0510N19	C 155	10	45.5	44	10	AV833060	AV833060	AV833060
C 83	10.8	49.1	43	9	AA932697	AA932697	co074d06.s	C 156	10	45.5	44	10	AV833060	AV833060	AV833060
C 84	10.8	49.1	43	9	AA932697	AA932697	co074d06.s	C 157	10	45.5	44	10	AV833060	AV833060	AV833060
C 85	10.8	49.1	43	9	AA974059	AA974059	co05h07.s	C 158	10	45.5	44	17	AZ509372	AZ509372	1M0352J17
C 86	10.8	49.1	43	9	AA974059	AA974059	co05h07.s	C 159	10	45.5	44	17	AZ509372	AZ509372	1M0352J17
C 87	10.8	49.1	44	13	BI860762	BI860762	603390194	C 160	10	45.5	45	14	T17560	T17560	mpe v16 The
C 88	10.8	49.1	44	13	BI860762	BI860762	603390194	C 161	10	45.5	45	17	AZ465721	AZ465721	1M0275014
C 89	10.8	49.1	44	17	BH865755	BH865755	SALK_0998	C 162	10	45.5	45	17	AZ465721	AZ465721	1M0275014
C 90	10.8	49.1	44	17	BH865755	BH865755	SALK_0998	C 163	10	45.5	46	9	AA705006	AA705006	zj95e12.s
C 91	10.8	49.1	47	13	BI151478	BI151478	602917488	C 164	10	45.5	46	9	AA705006	AA705006	zj95e12.s
C 92	10.8	49.1	47	13	BI151478	BI151478	602917488	C 165	10	45.5	46	9	AA705006	AA705006	zj95e12.s
C 93	10.8	49.1	50	9	AUI04929	AUI04929	AUI04929	C 166	10	45.5	46	9	AUI010025	AUI010025	AUI010025
C 94	10.8	49.1	50	9	AUI04929	AUI04929	AUI04929	C 167	10	45.5	46	9	AUI010025	AUI010025	AUI010025
C 95	10.8	49.1	50	9	AUI06987	AUI06987	AUI06987	C 168	10	45.5	48	12	BF035895	BF035895	601457806
C 96	10.8	49.1	50	9	AUI06987	AUI06987	AUI06987	C 169	10	45.5	49	13	BF035895	BF035895	601457806
C 97	10.8	49.1	50	12	BG118504	BG118504	602348435	C 170	10	45.5	49	13	BF035895	BF035895	601457806
C 98	10.8	49.1	50	12	BG118504	BG118504	602348435	C 171	10	45.5	50	9	AUI02324	AUI02324	AUI02324
C 99	10.8	49.1	50	12	BG178869	BG178869	602328026	C 172	10	45.5	50	9	AUI02324	AUI02324	AUI02324
C 100	10.8	49.1	50	12	BG178869	BG178869	602328026	C 173	10	45.5	50	9	AUI02324	AUI02324	AUI02324
C 101	10.6	48.2	22	17	AZ304010	AZ304010	1M0003023	C 174	10	45.5	50	9	AUI03849	AUI03849	AUI03849
C 102	10.6	48.2	22	17	AZ304010	AZ304010	1M0003023	C 175	10	45.5	50	9	AUI03849	AUI03849	AUI03849
C 103	10.6	48.2	28	17	BH864390	BH864390	SALK_0959	C 176	9.8	44.5	24	17	AZ367819	AZ367819	1M0117E05
C 104	10.6	48.2	28	17	BH864390	BH864390	SALK_0959	C 177	9.8	44.5	24	17	AZ367819	AZ367819	1M0117E05
C 105	10.6	48.2	38	17	BH864365	BH864365	SALK_0958	C 178	9.8	44.5	24	17	TA330F01Q	TA330F01Q	TA330F01Q
C 106	10.6	48.2	38	17	BH864365	BH864365	SALK_0958	C 179	9.8	44.5	24	17	TA330F01Q	TA330F01Q	TA330F01Q
C 107	10.6	48.2	44	17	AZ628166	AZ628166	1M0480C12	C 180	9.8	44.5	25	17	TA104C02Q	TA104C02Q	TA104C02Q
C 108	10.6	48.2	44	17	AZ628166	AZ628166	1M0480C12	C 181	9.8	44.5	25	17	TA104C02Q	TA104C02Q	TA104C02Q
C 109	10.6	48.2	45	17	AZ828142	AZ828142	2M0104P24	C 182	9.8	44.5	31	13	BI820240	BI820240	603037084
C 110	10.6	48.2	45	17	AZ828142	AZ828142	2M0104P24	C 183	9.8	44.5	31	13	BI820240	BI820240	603037084
C 111	10.6	48.2	50	9	AUI04287	AUI04287	AUI04287	C 184	9.8	44.5	33	10	AV957156	AV957156	AV957156
C 112	10.6	48.2	50	9	AUI04287	AUI04287	AUI04287	C 185	9.8	44.5	33	13	BM399063	BM399063	5009-0-52
C 113	10.4	47.3	32	13	BI739032	BI739032	603358882	C 186	9.8	44.5	33	13	BM399063	BM399063	5009-0-52
C 114	10.4	47.3	32	13	BI739032	BI739032	603358882	C 187	9.8	44.5	33	17	AZ352257	AZ352257	1M0090G11
C 115	10.4	47.3	35	17	AZ623458	AZ623458	1M0461D17	C 188	9.8	44.5	33	17	AZ352257	AZ352257	1M0090G11
C 116	10.4	47.3	35	17	AZ623458	AZ623458	1M0461D17	C 189	9.8	44.5	34	9	AA985167	AA985167	am79a09.s
C 117	10.4	47.3	36	9	AL646509	AL646509	AL646509	C 190	9.8	44.5	34	9	AA985167	AA985167	am79a09.s
C 118	10.4	47.3	36	9	AL646509	AL646509	AL646509	C 191	9.8	44.5	35	17	TA41H11P	TA41H11P	TA41H11P
C 119	10.4	47.3	50	9	AUI03395	AUI03395	AUI03395	C 192	9.8	44.5	35	17	TA41H11P	TA41H11P	TA41H11P
C 120	10.4	47.3	50	9	AUI03395	AUI03395	AUI03395	C 193	9.8	44.5	35	17	TA41H11P	TA41H11P	TA41H11P
C 121	10.4	47.3	50	9	AUI04123	AUI04123	AUI04123	C 194	9.8	44.5	39	17	AZ773780	AZ773780	2M0001E02
C 122	10.4	47.3	50	9	AUI04123	AUI04123	AUI04123	C 195	9.8	44.5	39	17	AZ773780	AZ773780	2M0001E02
C 123	10.4	47.3	50	9	AUI04496	AUI04496	AUI04496	C 196	9.8	44.5	43	17	BH740846	BH740846	KG05224-3
C 124	10.4	47.3	50	9	AUI04496	AUI04496	AUI04496	C 197	9.8	44.5	43	17	BH740846	BH740846	KG05224-3
C 125	10.2	46.4	43	9	AA011545	AA011545	z102d04.s	C 198	9.8	44.5	46	9	AI196701	AI196701	u153f07.y
C 126	10.2	46.4	43	9	AA011545	AA011545	z102d04.s	C 199	9.8	44.5	46	9	AI196701	AI196701	u153f07.y
C 127	10.2	46.4	50	9	AUI02352	AUI02352	AUI02352	C 200	9.8	44.5	47	9	AA642360	AA642360	ns29f08.s
C 128	10.2	46.4	50	9	AUI02352	AUI02352	AUI02352	C 201	9.8	44.5	47	17	BH631605	BH631605	100708560
C 129	10.2	46.4	50	9	AUI02353	AUI02353	AUI02353	C 202	9.8	44.5	47	17	BH631605	BH631605	100708560
C 130	10.2	46.4	50	9	AUI02353	AUI02353	AUI02353	C 203	9.8	44.5	48	17	BH811778	BH811778	SALK_0601
C 131	10.2	46.4	50	9	AUI02356	AUI02356	AUI02356	C 204	9.8	44.5	48	17	BH811778	BH811778	SALK_0601
C 132	10.2	46.4	50	9	AUI02356	AUI02356	AUI02356	C 205	9.8	44.5	49	9	AI004508	AI004508	oc66g10.s
C 133	10.2	46.4	50	9	AUI03419	AUI03419	AUI03419	C 206	9.8	44.5	49	9	AI004508	AI004508	oc66g10.s
C 134	10.2	46.4	50	9	AUI03419	AUI03419	AUI03419	C 207	9.8	44.5	49	17	AL752628	AL752628	Arabidops
C 135	10.2	46.4	50	9	AUI03713	AUI03713	AUI03713	C 208	9.8	44.5	49	17	AL752628	AL752628	Arabidops
C 136	10.2	46.4	50	9	AUI03713	AUI03713	AUI03713	C 209	9.8	44.5	50	9	AUI02274	AUI02274	AUI02274
C 137	10.2	46.4	50	9	AUI03714	AUI03714	AUI03714	C 210	9.8	44.5	50	9	AUI02274	AUI02274	AUI02274
C 138	10.2	46.4	50	9	AUI03714	AUI03714	AUI03714	C 211	9.8	44.5	50	9	AUI04024	AUI04024	AUI04024
C 139	10.2	46.4	50	9	AUI03715	AUI03715	AUI03715	C 212	9.8	44.5	50	9	AUI04024	AUI04024	AUI04024
C 140	10.2	46.4	50	9	AUI03715	AUI03715	AUI03715	C 213	9.8	44.5	50	9	AUI06341	AUI06341	AUI06341
C 141	10.2	46.4	50	9	AUI07979	AUI07979	AUI07979	C 214	9.8	44.5	50	9	AUI06341	AUI06341	AUI06341
C 142	10.2	46.4	50	9	AUI07979	AUI07979	AUI07979	C 215	9.8	44.5	50	10	AA689710	AA689710	NF023E07S
C 143	10	45.5	28	17	AZ843789	AZ843789	2M0142L15	C 216	9.8	44.5	50	10	AA689710	AA689710	NF023E07S
C 144	10	45.5	28	17	AZ843789	AZ843789	2M0142L15	C 217	9.6	43.6	24	17	TA245F07P	TA245F07P	TA245F07P
C 145	10	45.5	33	17	TA69G09P	TA69G09P	AL457596 T. brucei	C 218	9.6	43.6	24	17	TA245F07P	TA245F07P	TA245F07P
C 146	10	45.5	33	17	TA69G09P	TA69G09P	AL457596 T. brucei	C 219	9.6	43.6	27	14	T17528	T17528	gstr m60 The
C 147	10	45.5	40	12	BG777922	BG777922	602665676	C 220	9.6	43.6	27	14	T17528	T17528	gstr m60 The
C 148	10	45.5	40	12	BG777922	BG777922	602665676	C 221	9.6	43.6	27	17	TA02H07P	TA02H07P	TA02H07P
C 149	10	45.5	40	12	BG778865	BG778865	602667554	C 222	9.6	43.6	27	17	TA02H07P	TA02H07P	TA02H07P
C 150	10	45.5	40	12	BG778865	BG778865	602667554	C 223	9.6	43.6	28	17	TA196E08Q	TA196E08Q	TA196E08Q
C 151	10	45.5	40	17	AL756623	AL756623	Arabidops	C 224	9.6	43.6	28	17	TA196E08Q	TA196E08Q	TA196E08Q
C 152	10	45.5	40	17	AL756623	AL756623	Arabidops	C 225	9.6	43.6	30	17	AZ786502	AZ786502	2M0031A13

C 226	9.6	43.6	30	17	AZ786302	2M0031A13	299	9.4	42.7	45	17	TA129F11P	AL464009 T. brucei
C 227	9.6	43.6	39	17	AL752652	Arabidops	C 300	9.4	42.7	45	17	TA129F11P	AL464009 T. brucei
C 228	9.6	43.6	39	17	AL752652	Arabidops	C 301	9.4	42.7	46	17	TA129F11P	AA064198
C 229	9.6	43.6	43	9	AA200880	mu03b12.r	C 302	9.4	42.7	46	9	AA064198	AA064198 mj62d12.r
C 230	9.6	43.6	43	9	AA200880	mu03b12.r	C 303	9.4	42.7	46	14	T80386	T80386 yd05d03.r1
C 231	9.6	43.6	46	14	N75232	yz73d12.r1	C 304	9.4	42.7	46	14	T80386	T80386 yd05d03.r1
C 232	9.6	43.6	48	14	N75232	yz73d12.r1	C 305	9.4	42.7	47	17	BH795957	BH795957 1008092B0
C 233	9.6	43.6	48	10	AV841288	AV841288	C 306	9.4	42.7	47	17	BH795957	BH795957 1008092B0
C 234	9.6	43.6	49	10	AV841288	AV841288	C 307	9.4	42.7	47	17	TA220G01P	AL480235 T. brucei
C 235	9.6	43.6	49	9	AT756242	EESTea41	C 308	9.4	42.7	47	17	TA220G01P	AL480235 T. brucei
C 236	9.6	43.6	49	9	AT756242	EESTea41	C 309	9.4	42.7	48	17	AZ830212	AZ830212 2M0109M16
C 237	9.6	43.6	49	13	B1518984	603062281	C 310	9.4	42.7	48	17	AZ830212	AZ830212 2M0109M16
C 238	9.6	43.6	49	13	B1518984	603062281	C 311	9.4	42.7	50	9	AU102347	AU102347 AU102347
C 239	9.6	43.6	50	9	AU104277	AU104277	C 312	9.4	42.7	50	9	AU102347	AU102347 AU102347
C 240	9.6	43.6	50	9	AU104277	AU104277	C 313	9.4	42.7	50	9	AU104211	AU104211 AU104211
C 241	9.6	43.6	50	9	AU106352	AU106352	C 314	9.4	42.7	50	9	AU104321	AU104321 AU104321
C 242	9.6	43.6	50	9	AU106352	AU106352	C 315	9.4	42.7	50	9	AU104332	AU104332 AU104332
C 243	9.6	43.6	50	9	AU107994	AU107994	C 316	9.4	42.7	50	9	AU104352	AU104352 AU104352
C 244	9.6	43.6	50	9	AU107994	AU107994	C 317	9.4	42.7	50	9	AU107136	AU107136 AU107136
C 245	9.4	42.7	25	14	L32057	HUMKPG6GA H	C 318	9.4	42.7	50	9	AU107137	AU107137 AU107137
C 246	9.4	42.7	25	14	L32057	HUMKPG6GA H	C 319	9.4	42.7	50	9	AU107137	AU107137 AU107137
C 247	9.4	42.7	29	9	AU012322	AU012322	C 320	9.4	42.7	50	9	AU107139	AU107139 AU107139
C 248	9.4	42.7	29	9	AU012322	AU012322	C 321	9.4	42.7	50	9	AU107139	AU107139 AU107139
C 249	9.4	42.7	30	9	AU012182	AU012182	C 322	9.4	42.7	50	9	AU107140	AU107140 AU107140
C 250	9.4	42.7	30	9	AU012182	AU012182	C 323	9.4	42.7	50	9	AU107140	AU107140 AU107140
C 251	9.4	42.7	30	9	AU256792	AU256792	C 324	9.4	42.7	50	9	AU107141	AU107141 AU107141
C 252	9.4	42.7	30	9	AU256792	AU256792	C 325	9.4	42.7	50	9	AU107141	AU107141 AU107141
C 253	9.4	42.7	31	17	AZ610795	1M0436H19	C 326	9.4	42.7	50	9	AU107142	AU107142 AU107142
C 254	9.4	42.7	31	17	AZ610795	1M0436H19	C 327	9.4	42.7	50	9	AU107142	AU107142 AU107142
C 255	9.4	42.7	31	17	AZ610795	1M0436H19	C 328	9.4	42.7	50	9	AU107142	AU107142 AU107142
C 256	9.4	42.7	31	17	AZ610795	1M0436H19	C 329	9.4	42.7	50	9	AU107187	AU107187 AU107187
C 257	9.4	42.7	31	17	TA13E07P	AL452354 T. brucei	C 330	9.4	42.7	50	9	AU107187	AU107187 AU107187
C 258	9.4	42.7	32	17	TA13E07P	AL452354 T. brucei	C 331	9.4	42.7	50	9	AU107626	AU107626 AU107626
C 259	9.4	42.7	34	17	AA436781	zV70910.r	C 332	9.4	42.7	50	9	AU107626	AU107626 AU107626
C 260	9.4	42.7	34	17	AA436781	zV70910.r	C 333	9.4	42.7	50	13	B1335418	B1335418 602998302
C 261	9.4	42.7	35	17	AZ428773	1M0212123	C 334	9.4	42.7	50	13	B1335418	B1335418 602998302
C 262	9.4	42.7	35	17	AZ428773	1M0212123	C 335	9.4	42.7	50	14	BQ789776	BQ789776 hage002aA
C 263	9.4	42.7	36	17	BH792341	SAUK_0640	C 336	9.2	41.8	20	14	BQ789776	BQ789776 hage002aA
C 264	9.4	42.7	36	17	BH792341	SAUK_0640	C 337	9.2	41.8	25	17	AZ655084	AZ655084 1M0529C20
C 265	9.4	42.7	37	9	AT120995	ub75f11.r	C 338	9.2	41.8	25	17	AZ655084	AZ655084 1M0529C20
C 266	9.4	42.7	37	9	AT120995	ub75f11.r	C 339	9.2	41.8	26	17	BH791427	BH791427 SAUK_0599
C 267	9.4	42.7	37	9	AA275360	vc07d04.r	C 340	9.2	41.8	26	17	BH791427	BH791427 SAUK_0599
C 268	9.4	42.7	37	9	AA275360	vc07d04.r	C 341	9.2	41.8	29	17	AZ683393	AZ683393 2M0171D04
C 269	9.4	42.7	38	9	AU259167	AU259167	C 342	9.2	41.8	29	17	AZ683393	AZ683393 2M0171D04
C 270	9.4	42.7	38	9	AU259167	AU259167	C 343	9.2	41.8	30	17	AL769095	AL769095 Arabidops
C 271	9.4	42.7	38	13	BJ015013	BJ015013	C 344	9.2	41.8	30	17	AL769095	AL769095 Arabidops
C 272	9.4	42.7	38	13	BJ015013	BJ015013	C 345	9.2	41.8	33	17	BH791695	BH791695 SAUK_0608
C 273	9.4	42.7	39	9	AU011691	AU011691	C 346	9.2	41.8	33	17	BH791695	BH791695 SAUK_0608
C 274	9.4	42.7	39	9	AU011691	AU011691	C 347	9.2	41.8	34	17	TA210F03Q	AL478781 T. brucei
C 275	9.4	42.7	39	17	AZ310708	1M0025J16	C 348	9.2	41.8	34	17	TA210F03Q	AL478781 T. brucei
C 276	9.4	42.7	39	17	AZ310708	1M0025J16	C 349	9.2	41.8	35	17	AZ499700	AZ499700 1M0337F11
C 277	9.4	42.7	40	9	AT1570731	ct66c01.x	C 350	9.2	41.8	35	17	AZ499700	AZ499700 1M0337F11
C 278	9.4	42.7	40	9	AT1570731	ct66c01.x	C 351	9.2	41.8	36	12	BF159227	BF159227 601766682
C 279	9.4	42.7	40	9	AT1761272	w168h04.x	C 352	9.2	41.8	36	12	BF159227	BF159227 601766682
C 280	9.4	42.7	40	9	AT1761272	w168h04.x	C 353	9.2	41.8	36	17	AZ619194	AZ619194 1M0451J19
C 281	9.4	42.7	40	17	AZ772376	1M0583011	C 354	9.2	41.8	36	17	AZ619194	AZ619194 1M0451J19
C 282	9.4	42.7	40	17	AZ772376	1M0583011	C 355	9.2	41.8	36	17	BH812173	BH812173 SAUK_0613
C 283	9.4	42.7	40	17	CNS07EUR	Arabidops	C 356	9.2	41.8	36	17	BH812173	BH812173 SAUK_0613
C 284	9.4	42.7	40	17	CNS07EUR	Arabidops	C 357	9.2	41.8	37	10	AV847617	AV847617 AV847617
C 285	9.4	42.7	42	12	BG751431	602730004	C 358	9.2	41.8	37	10	AV847617	AV847617 AV847617
C 286	9.4	42.7	42	12	BG751431	602730004	C 359	9.2	41.8	38	17	AO025575	AO025575 fs(3)0564
C 287	9.4	42.7	42	17	AZ318518	1M0037D04	C 360	9.2	41.8	40	9	AA588339	AA588339 tm93D07.s
C 288	9.4	42.7	42	17	AZ318518	1M0037D04	C 361	9.2	41.8	40	9	AA588339	AA588339 tm93D07.s
C 289	9.4	42.7	42	17	AL762458	Arabidops	C 362	9.2	41.8	40	9	AA588339	AA588339 tm93D07.s
C 290	9.4	42.7	42	17	AL762458	Arabidops	C 363	9.2	41.8	40	17	DRe120T	AL735119 Danio rer
C 291	9.4	42.7	43	9	AT1098967	ub99g04.r	C 364	9.2	41.8	40	17	DRe120T	AL735119 Danio rer
C 292	9.4	42.7	43	9	AT1098967	ub99g04.r	C 365	9.2	41.8	41	13	BJ062022	BJ062022 BJ062022
C 293	9.4	42.7	43	17	AZ592609	1M0403F12	C 366	9.2	41.8	41	13	BJ062022	BJ062022 BJ062022
C 294	9.4	42.7	43	17	AZ592609	1M0403F12	C 367	9.2	41.8	41	17	BH863791	BH863791 SAUK_0946
C 295	9.4	42.7	44	9	AU254864	AU254864	C 368	9.2	41.8	41	17	BH863791	BH863791 SAUK_0946
C 296	9.4	42.7	44	9	AU254864	AU254864	C 369	9.2	41.8	42	10	AV833675	AV833675 AV833675
C 297	9.4	42.7	44	13	BJ033903	BJ033903	C 370	9.2	41.8	42	10	AV833675	AV833675 AV833675
C 298	9.4	42.7	44	13	BJ033903	BJ033903	C 371	9.2	41.8	43	9	AI152426	AI152426 ud91g05.r

C 372	9.2	41.8	43	9	A1152426	A1152426 u491905.r	445	9.2	41.8	50	9	AU103140	AU103140
C 373	9.2	41.8	44	14	R23375	R23375 yh33f01.s1	C 446	9.2	41.8	50	9	AU103140	AU103140
C 374	9.2	41.8	44	14	R23375	R23375 yh33f01.s1	C 447	9.2	41.8	50	9	AU103141	AU103141
C 375	9.2	41.8	44	17	AZ825920	AZ825920 2M0101C23	C 448	9.2	41.8	50	9	AU103141	AU103141
C 376	9.2	41.8	44	17	AZ825920	AZ825920 2M0101C23	C 449	9.2	41.8	50	9	AU103142	AU103142
C 377	9.2	41.8	44	17	BH862329	BH862329 SALK_0893	C 450	9.2	41.8	50	9	AU103142	AU103142
C 378	9.2	41.8	44	17	BH862329	BH862329 SALK_0893	C 451	9.2	41.8	50	9	AU103144	AU103144
C 379	9.2	41.8	45	17	AZ307664	AZ307664 1M0009J21	C 452	9.2	41.8	50	9	AU103144	AU103144
C 380	9.2	41.8	45	17	AZ307664	AZ307664 1M0009J21	C 453	9.2	41.8	50	9	AU103145	AU103145
C 381	9.2	41.8	45	17	BH812636	BH812636 SALK_0622	C 454	9.2	41.8	50	9	AU103145	AU103145
C 382	9.2	41.8	45	17	BH812636	BH812636 SALK_0622	C 455	9.2	41.8	50	9	AU103146	AU103146
C 383	9.2	41.8	46	14	R05843	R05843 ye88e10.r1	C 456	9.2	41.8	50	9	AU103146	AU103146
C 384	9.2	41.8	46	14	R05843	R05843 ye88e10.r1	C 457	9.2	41.8	50	9	AU103245	AU103245
C 385	9.2	41.8	46	14	R41260	R41260 yf85a04.s1	C 458	9.2	41.8	50	9	AU103245	AU103245
C 386	9.2	41.8	46	14	R41260	R41260 yf85a04.s1	C 459	9.2	41.8	50	9	AU103969	AU103969
C 387	9.2	41.8	46	17	AL769815	AL769815 Arabidops	C 460	9.2	41.8	50	9	AU104155	AU104155
C 388	9.2	41.8	46	17	AL769815	AL769815 Arabidops	C 461	9.2	41.8	50	9	AU104155	AU104155
C 389	9.2	41.8	48	13	BJ000382	BJ000382 BJ000382	C 462	9.2	41.8	50	9	AU104155	AU104155
C 390	9.2	41.8	48	13	BJ000382	BJ000382 BJ000382	C 463	9.2	41.8	50	9	AU104252	AU104252
C 391	9.2	41.8	49	9	AA789791	AA789791 vt79d11.r	C 464	9.2	41.8	50	9	AU104252	AU104252
C 392	9.2	41.8	49	9	AA789791	AA789791 vt79d11.r	C 465	9.2	41.8	50	9	AU104254	AU104254
C 393	9.2	41.8	50	9	AU103108	AU103108 AU103108	C 466	9.2	41.8	50	9	AU104254	AU104254
C 394	9.2	41.8	50	9	AU103108	AU103108 AU103108	C 467	9.2	41.8	50	9	AU105016	AU105016
C 395	9.2	41.8	50	9	AU103109	AU103109 AU103109	C 468	9.2	41.8	50	9	AU105016	AU105016
C 396	9.2	41.8	50	9	AU103109	AU103109 AU103109	C 469	9.2	41.8	50	9	AU105082	AU105082
C 397	9.2	41.8	50	9	AU103110	AU103110 AU103110	C 470	9.2	41.8	50	9	AU105082	AU105082
C 398	9.2	41.8	50	9	AU103110	AU103110 AU103110	C 471	9.2	41.8	50	9	AU105212	AU105212
C 399	9.2	41.8	50	9	AU103111	AU103111 AU103111	C 472	9.2	41.8	50	9	AU105472	AU105472
C 400	9.2	41.8	50	9	AU103111	AU103111 AU103111	C 473	9.2	41.8	50	9	AU105472	AU105472
C 401	9.2	41.8	50	9	AU103113	AU103113 AU103113	C 474	9.2	41.8	50	9	AU105473	AU105473
C 402	9.2	41.8	50	9	AU103113	AU103113 AU103113	C 475	9.2	41.8	50	9	AU105473	AU105473
C 403	9.2	41.8	50	9	AU103114	AU103114 AU103114	C 476	9.2	41.8	50	9	AU105474	AU105474
C 404	9.2	41.8	50	9	AU103115	AU103115 AU103115	C 477	9.2	41.8	50	9	AU105474	AU105474
C 405	9.2	41.8	50	9	AU103115	AU103115 AU103115	C 478	9.2	41.8	50	9	AU105475	AU105475
C 406	9.2	41.8	50	9	AU103115	AU103115 AU103115	C 479	9.2	41.8	50	9	AU105475	AU105475
C 407	9.2	41.8	50	9	AU103116	AU103116 AU103116	C 480	9.2	41.8	50	9	AU105476	AU105476
C 408	9.2	41.8	50	9	AU103116	AU103116 AU103116	C 481	9.2	41.8	50	9	AU105476	AU105476
C 409	9.2	41.8	50	9	AU103117	AU103117 AU103117	C 482	9.2	41.8	50	9	AU105479	AU105479
C 410	9.2	41.8	50	9	AU103117	AU103117 AU103117	C 483	9.2	41.8	50	9	AU105479	AU105479
C 411	9.2	41.8	50	9	AU103118	AU103118 AU103118	C 484	9.2	41.8	50	9	AU105480	AU105480
C 412	9.2	41.8	50	9	AU103118	AU103118 AU103118	C 485	9.2	41.8	50	9	AU105480	AU105480
C 413	9.2	41.8	50	9	AU103119	AU103119 AU103119	C 486	9.2	41.8	50	9	AU105480	AU105480
C 414	9.2	41.8	50	9	AU103119	AU103119 AU103119	C 487	9.2	41.8	50	9	AU105862	AU105862
C 415	9.2	41.8	50	9	AU103121	AU103121 AU103121	C 488	9.2	41.8	50	9	AU105862	AU105862
C 416	9.2	41.8	50	9	AU103121	AU103121 AU103121	C 489	9.2	41.8	50	9	AU106400	AU106400
C 417	9.2	41.8	50	9	AU103123	AU103123 AU103123	C 490	9.2	41.8	50	9	AU106400	AU106400
C 418	9.2	41.8	50	9	AU103123	AU103123 AU103123	C 491	9.2	41.8	50	9	AU106401	AU106401
C 419	9.2	41.8	50	9	AU103124	AU103124 AU103124	C 492	9.2	41.8	50	9	AU106401	AU106401
C 420	9.2	41.8	50	9	AU103124	AU103124 AU103124	C 493	9.2	41.8	50	9	AU106403	AU106403
C 421	9.2	41.8	50	9	AU103125	AU103125 AU103125	C 494	9.2	41.8	50	9	AU106403	AU106403
C 422	9.2	41.8	50	9	AU103125	AU103125 AU103125	C 495	9.2	41.8	50	9	AU106404	AU106404
C 423	9.2	41.8	50	9	AU103127	AU103127 AU103127	C 496	9.2	41.8	50	9	AU106404	AU106404
C 424	9.2	41.8	50	9	AU103127	AU103127 AU103127	C 497	9.2	41.8	50	9	AU106408	AU106408
C 425	9.2	41.8	50	9	AU103128	AU103128 AU103128	C 498	9.2	41.8	50	9	AU106408	AU106408
C 426	9.2	41.8	50	9	AU103128	AU103128 AU103128	C 499	9.2	41.8	50	9	AU106409	AU106409
C 427	9.2	41.8	50	9	AU103129	AU103129 AU103129	C 500	9.2	41.8	50	9	AU106409	AU106409
C 428	9.2	41.8	50	9	AU103129	AU103129 AU103129	C 501	9.2	41.8	50	9	AU106410	AU106410
C 429	9.2	41.8	50	9	AU103130	AU103130 AU103130	C 502	9.2	41.8	50	9	AU106410	AU106410
C 430	9.2	41.8	50	9	AU103130	AU103130 AU103130	C 503	9.2	41.8	50	9	AU106412	AU106412
C 431	9.2	41.8	50	9	AU103131	AU103131 AU103131	C 504	9.2	41.8	50	9	AU106412	AU106412
C 432	9.2	41.8	50	9	AU103131	AU103131 AU103131	C 505	9.2	41.8	50	9	AU106419	AU106419
C 433	9.2	41.8	50	9	AU103132	AU103132 AU103132	C 506	9.2	41.8	50	9	AU106419	AU106419
C 434	9.2	41.8	50	9	AU103132	AU103132 AU103132	C 507	9.2	41.8	50	9	AU106421	AU106421
C 435	9.2	41.8	50	9	AU103133	AU103133 AU103133	C 508	9.2	41.8	50	9	AU106421	AU106421
C 436	9.2	41.8	50	9	AU103133	AU103133 AU103133	C 509	9.2	41.8	50	9	AU106425	AU106425
C 437	9.2	41.8	50	9	AU103134	AU103134 AU103134	C 510	9.2	41.8	50	9	AU106425	AU106425
C 438	9.2	41.8	50	9	AU103134	AU103134 AU103134	C 511	9.2	41.8	50	9	AU106430	AU106430
C 439	9.2	41.8	50	9	AU103135	AU103135 AU103135	C 512	9.2	41.8	50	9	AU106430	AU106430
C 440	9.2	41.8	50	9	AU103135	AU103135 AU103135	C 513	9.2	41.8	50	9	AU106432	AU106432
C 441	9.2	41.8	50	9	AU103138	AU103138 AU103138	C 514	9.2	41.8	50	9	AU106432	AU106432
C 442	9.2	41.8	50	9	AU103138	AU103138 AU103138	C 515	9.2	41.8	50	9	AU106433	AU106433
C 443	9.2	41.8	50	9	AU103139	AU103139 AU103139	C 516	9.2	41.8	50	9	AU106433	AU106433
C 444	9.2	41.8	50	9	AU103139	AU103139 AU103139	C 517	9.2	41.8	50	9	AU106435	AU106435

C 518	9.2	41.8	50	9	AUI06435	AUI06435	591	9	40.9	32	17	TA60B12Q	AL455905 T. brucei
C 519	9.2	41.8	50	9	AUI06438	AUI06438	C 592	9	40.9	32	17	TA60B12Q	AL455905 T. brucei
C 520	9.2	41.8	50	9	AUI06438	AUI06438	C 593	9	40.9	34	17	TA60B12Q	AL455905 T. brucei
C 521	9.2	41.8	50	9	AUI06442	AUI06442	C 594	9	40.9	34	17	AZ769429	AZ769429 IM0570B09
C 522	9.2	41.8	50	9	AUI06442	AUI06442	C 595	9	40.9	34	17	AZ769429	AZ769429 IM0570B09
C 523	9.2	41.8	50	9	AUI06444	AUI06444	C 596	9	40.9	34	17	BH865779	BH865779 SALK_0998
C 524	9.2	41.8	50	9	AUI06444	AUI06444	C 597	9	40.9	34	17	BH865779	BH865779 SALK_0998
C 525	9.2	41.8	50	9	AUI06446	AUI06446	C 598	9	40.9	36	17	TA100G04Q	AL459362 T. brucei
C 526	9.2	41.8	50	9	AUI06446	AUI06446	C 599	9	40.9	36	17	TA100G04Q	AL459362 T. brucei
C 527	9.2	41.8	50	9	AUI06449	AUI06449	C 600	9	40.9	37	9	AL677081	AL677081 AL677081
C 528	9.2	41.8	50	9	AUI06449	AUI06449	C 601	9	40.9	37	17	AL753259	AL753259 Arabidops
C 529	9.2	41.8	50	9	AUI06452	AUI06452	C 602	9	40.9	37	17	AL753259	AL753259 Arabidops
C 530	9.2	41.8	50	9	AUI06452	AUI06452	C 603	9	40.9	38	17	AQ025901	AQ025901 1(2)K0962
C 531	9.2	41.8	50	9	AUI06459	AUI06459	C 604	9	40.9	38	17	AQ025901	AQ025901 1(2)K0962
C 532	9.2	41.8	50	9	AUI06459	AUI06459	C 605	9	40.9	39	10	BE544028	BE544028 601069976
C 533	9.2	41.8	50	9	AUI06460	AUI06460	C 606	9	40.9	39	10	BE544028	BE544028 601069976
C 534	9.2	41.8	50	9	AUI06460	AUI06460	C 607	9	40.9	40	9	AI366718	AI366718 QY95B09.x
C 535	9.2	41.8	50	9	AUI06467	AUI06467	C 608	9	40.9	40	9	AI366718	AI366718 QY95B09.x
C 536	9.2	41.8	50	9	AUI06467	AUI06467	C 609	9	40.9	40	9	AA237539	AA237539 mx28e06.r
C 537	9.2	41.8	50	9	AUI06498	AUI06498	C 610	9	40.9	40	9	AA237539	AA237539 mx28e06.r
C 538	9.2	41.8	50	9	AUI06498	AUI06498	C 611	9	40.9	40	13	BJ066312	BJ066312 BJ066312
C 539	9.2	41.8	50	9	AUI06499	AUI06499	C 612	9	40.9	40	13	BJ066312	BJ066312 Arabidops
C 540	9.2	41.8	50	9	AUI06499	AUI06499	C 613	9	40.9	40	17	AL753351	AL753351 Arabidops
C 541	9.2	41.8	50	9	AUI06504	AUI06504	C 614	9	40.9	40	17	AL753351	AL753351 Arabidops
C 542	9.2	41.8	50	9	AUI06504	AUI06504	C 615	9	40.9	41	12	BC472622	BC472622 602514402
C 543	9.2	41.8	50	9	AUI06505	AUI06505	C 616	9	40.9	41	12	BC472622	BC472622 602514402
C 544	9.2	41.8	50	9	AUI06505	AUI06505	C 617	9	40.9	42	17	AZ472668	AZ472668 1M0288G03
C 545	9.2	41.8	50	9	AUI06507	AUI06507	C 618	9	40.9	42	17	AZ472668	AZ472668 1M0288G03
C 546	9.2	41.8	50	9	AUI06507	AUI06507	C 619	9	40.9	43	17	BH891787	BH891787 3526_1-19
C 547	9.2	41.8	50	9	AUI06508	AUI06508	C 620	9	40.9	43	17	BH891787	BH891787 3526_1-19
C 548	9.2	41.8	50	9	AUI06508	AUI06508	C 621	9	40.9	44	17	AQ025716	AQ025716 1(2)K0280
C 549	9.2	41.8	50	9	AUI06510	AUI06510	C 622	9	40.9	44	17	AQ025716	AQ025716 1(2)K0280
C 550	9.2	41.8	50	9	AUI06510	AUI06510	C 623	9	40.9	45	14	H67715	H67715 Yr72c07.s1
C 551	9.2	41.8	50	9	AUI06511	AUI06511	C 624	9	40.9	45	14	H67715	H67715 Yr72c07.s1
C 552	9.2	41.8	50	9	AUI06511	AUI06511	C 625	9	40.9	46	17	TA212P10Q	AL479585 T. brucei
C 553	9.2	41.8	50	9	AUI06514	AUI06514	C 626	9	40.9	46	17	TA212P10Q	AL479585 T. brucei
C 554	9.2	41.8	50	9	AUI06514	AUI06514	C 627	9	40.9	48	17	AZ602280	AZ602280 IM0420P21
C 555	9.2	41.8	50	9	AUI06526	AUI06526	C 628	9	40.9	48	17	AZ602280	AZ602280 IM0420P21
C 556	9.2	41.8	50	9	AUI06526	AUI06526	C 629	9	40.9	49	12	BF034811	BF034811 601457315
C 557	9.2	41.8	50	9	AUI06527	AUI06527	C 630	9	40.9	49	12	BF034811	BF034811 601457315
C 558	9.2	41.8	50	9	AUI06527	AUI06527	C 631	9	40.9	49	17	BH803126	BH803126 100810051
C 559	9.2	41.8	50	9	AUI06528	AUI06528	C 632	9	40.9	49	17	BH803126	BH803126 100810051
C 560	9.2	41.8	50	9	AUI06528	AUI06528	C 633	9	40.9	49	17	BH855856	BH855856 SALK_0844
C 561	9.2	41.8	50	9	AUI06530	AUI06530	C 634	9	40.9	49	17	BH855856	BH855856 SALK_0844
C 562	9.2	41.8	50	9	AUI06530	AUI06530	C 635	9	40.9	49	17	BH855857	BH855857 SALK_0844
C 563	9.2	41.8	50	9	AUI06531	AUI06531	C 636	9	40.9	49	17	BH855857	BH855857 SALK_0844
C 564	9.2	41.8	50	9	AUI06531	AUI06531	C 637	9	40.9	50	9	AUI02673	AUI02673 AUI02673
C 565	9.2	41.8	50	9	AUI06532	AUI06532	C 638	9	40.9	50	9	AUI02673	AUI02673 AUI02673
C 566	9.2	41.8	50	9	AUI06532	AUI06532	C 639	9	40.9	50	9	AUI03412	AUI03412 AUI03412
C 567	9.2	41.8	50	9	AUI06533	AUI06533	C 640	9	40.9	50	9	AUI03412	AUI03412 AUI03412
C 568	9.2	41.8	50	9	AUI06533	AUI06533	C 641	9	40.9	50	9	AUI03627	AUI03627 AUI03627
C 569	9.2	41.8	50	9	AUI06534	AUI06534	C 642	9	40.9	50	9	AUI03627	AUI03627 AUI03627
C 570	9.2	41.8	50	9	AUI06534	AUI06534	C 643	9	40.9	50	9	AUI03925	AUI03925 AUI03925
C 571	9.2	41.8	50	9	AUI06536	AUI06536	C 644	9	40.9	50	9	AUI03925	AUI03925 AUI03925
C 572	9.2	41.8	50	9	AUI06536	AUI06536	C 645	9	40.9	50	9	AUI03979	AUI03979 AUI03979
C 573	9.2	41.8	50	9	AUI06537	AUI06537	C 646	9	40.9	50	9	AUI03979	AUI03979 AUI03979
C 574	9.2	41.8	50	9	AUI06537	AUI06537	C 647	9	40.9	50	9	AUI04912	AUI04912 AUI04912
C 575	9.2	41.8	50	9	AUI06539	AUI06539	C 648	9	40.9	50	9	AUI04912	AUI04912 AUI04912
C 576	9.2	41.8	50	9	AUI06539	AUI06539	C 649	9	40.9	50	9	AUI07941	AUI07941 AUI07941
C 577	9.2	41.8	50	9	AUI06543	AUI06543	C 650	9	40.9	50	9	AUI07941	AUI07941 AUI07941
C 578	9.2	41.8	50	9	AUI06543	AUI06543	C 651	9	40.9	50	9	AA430812	AA430812 RRAMCA153
C 579	9.2	41.8	50	9	AUI07046	AUI07046	C 652	9	40.9	50	9	AA430812	AA430812 RRAMCA153
C 580	9.2	41.8	50	9	AUI07046	AUI07046	C 653	9	40.9	50	17	AZ8220525	AZ8220525 2M0092E10
C 581	9	40.9	20	13	BM393606	BM393606	C 654	9	40.9	50	17	AZ8220525	AZ8220525 2M0092E10
C 582	9	40.9	20	13	BM393606	BM393606	C 655	9	40.9	50	17	TA374G11Q	TA374G11Q T. brucei
C 583	9	40.9	25	17	AZ810962	AZ810962	C 656	9	40.9	50	17	TA374G11Q	TA374G11Q T. brucei
C 584	9	40.9	25	17	AZ810962	AZ810962	C 657	9	40.9	17	13	BM399854	BM399854 5009-0-5-
C 585	9	40.9	29	17	BH861244	BH861244	C 658	9	40.0	17	13	BM399854	BM399854 5009-0-5-
C 586	9	40.9	29	17	BH861245	BH861245	C 659	9	40.0	25	10	AM246508	AM246508 2821703.3
C 587	9	40.9	29	17	BH861245	BH861245	C 660	9	40.0	25	10	AM246508	AM246508 2821703.3
C 588	9	40.9	29	17	BH861245	BH861245	C 661	9	40.0	25	17	AZ464201	AZ464201 IM0273P24
C 589	9	40.9	31	9	AI493525	AI493525	C 662	9	40.0	25	17	AZ464201	AZ464201 IM0273P24
C 590	9	40.9	31	9	AI493525	AI493525	C 663	9	40.0	25	17	TA132G12P	TA132G12P T. brucei

C 664	8.8	40.0	25	17	TA132G12P	AL45564 T. brucei	737	8.8	40.0	43	9	A1789878	A1789878 ue65f10.r
C 665	8.8	40.0	27	2	HSM007348	A1042498 Homo sapi	C 738	8.8	40.0	43	9	A1789878	A1789878 ue65f10.r
C 666	8.8	40.0	27	2	HSM007348	A1042498 Homo sapi	C 739	8.8	40.0	43	10	AM064197	AM064197 SP0644 KR
C 667	8.8	40.0	28	2	HSM007350	A1042500 Homo sapi	C 740	8.8	40.0	43	10	AM064197	AM064197 SP0644 KR
C 668	8.8	40.0	28	2	HSM007350	A1042500 Homo sapi	C 741	8.8	40.0	43	14	C00370	C00370 HMG0000366
C 669	8.8	40.0	29	17	AZ966795	AZ966795 2M0237P23	C 742	8.8	40.0	43	14	C00370	C00370 HMG0000366
C 670	8.8	40.0	29	17	AZ966795	AZ966795 2M0237P23	C 743	8.8	40.0	43	17	AZ305746	AZ305746 1M0006306
C 671	8.8	40.0	31	17	BH791422	BH791422 SALK_0599	C 744	8.8	40.0	43	17	AZ305746	AZ305746 1M0006306
C 672	8.8	40.0	31	17	BH791422	BH791422 SALK_0599	C 745	8.8	40.0	43	17	AZ575514	AZ575514 AST-T21F0
C 673	8.8	40.0	32	17	AL754213	AL754213 Arabidops	C 746	8.8	40.0	43	17	AZ575514	AZ575514 AST-T21F0
C 674	8.8	40.0	32	17	AL754213	AL754213 Arabidops	C 747	8.8	40.0	43	17	AZ784062	AZ784062 2M0026M21
C 675	8.8	40.0	33	17	AZ458451	AZ458451 1M0262L01	C 748	8.8	40.0	43	17	AZ784062	AZ784062 2M0026M21
C 676	8.8	40.0	33	17	AZ458451	AZ458451 1M0262L01	C 749	8.8	40.0	43	17	AZ842357	AZ842357 2M0140J16
C 677	8.8	40.0	34	9	AA988881	AA988881 or86d09.s	C 750	8.8	40.0	43	17	AZ842357	AZ842357 2M0140J16
C 678	8.8	40.0	34	9	AA988881	AA988881 or86d09.s	C 751	8.8	40.0	43	17	BH892666	BH892666 3526_1.22
C 679	8.8	40.0	34	12	BF576427	BF576427 602133840	C 752	8.8	40.0	43	17	BH892666	BH892666 3526_1.22
C 680	8.8	40.0	34	12	BF576427	BF576427 602133840	C 753	8.8	40.0	44	12	BG779515	BG779515 602666932
C 681	8.8	40.0	35	9	AU244156	AU244156 AU244156	C 754	8.8	40.0	44	12	BG779515	BG779515 602666932
C 682	8.8	40.0	35	9	AU244156	AU244156 AU244156	C 755	8.8	40.0	44	17	AZ784742	AZ784742 2M0027006
C 683	8.8	40.0	35	12	BG529663	BG529663 602558102	C 756	8.8	40.0	44	17	AZ784742	AZ784742 2M0027006
C 684	8.8	40.0	35	12	BG529663	BG529663 602558102	C 757	8.8	40.0	44	17	AZ784742	AZ784742 2M0027006
C 685	8.8	40.0	36	12	BF790288	BF790288 602249513	C 758	8.8	40.0	44	17	AZ784742	AZ784742 2M0027006
C 686	8.8	40.0	36	12	BF790288	BF790288 602249513	C 759	8.8	40.0	44	17	AZ784742	AZ784742 2M0027006
C 687	8.8	40.0	36	14	C00778	C00778 HUMG000239	C 760	8.8	40.0	44	17	AZ784742	AZ784742 2M0027006
C 688	8.8	40.0	36	14	C00778	C00778 HUMG000239	C 761	8.8	40.0	45	10	AV844706	AV844706 AV844706
C 689	8.8	40.0	36	14	H45291	H45291 yn99d02.s1	C 762	8.8	40.0	45	10	AV844706	AV844706 AV844706
C 690	8.8	40.0	36	14	H45291	H45291 yn99d02.s1	C 763	8.8	40.0	45	13	B1067044	B1067044 B1067044
C 691	8.8	40.0	36	17	BH789699	BH789699 SALK_0444	C 764	8.8	40.0	45	13	B1067044	B1067044 B1067044
C 692	8.8	40.0	36	17	BH789699	BH789699 SALK_0444	C 765	8.8	40.0	45	14	D45793	D45793 HUMG003008
C 693	8.8	40.0	36	17	BH857872	BH857872 SALK_0875	C 766	8.8	40.0	45	14	D45793	D45793 HUMG003008
C 694	8.8	40.0	36	17	BH857872	BH857872 SALK_0875	C 767	8.8	40.0	45	17	AZ432380	AZ432380 1M0217H13
C 695	8.8	40.0	37	9	AA681821	AA681821 vub5h03.r	C 768	8.8	40.0	45	17	AZ432380	AZ432380 1M0217H13
C 696	8.8	40.0	37	9	AA681821	AA681821 vub5h03.r	C 769	8.8	40.0	45	17	BH759240	BH759240 KG00542-3
C 697	8.8	40.0	37	9	AA681821	AA681821 vub5h03.r	C 770	8.8	40.0	45	17	BH759240	BH759240 KG00542-3
C 698	8.8	40.0	37	9	AA135712	AA135712 qv17h02.x	C 771	8.8	40.0	45	17	BH759240	BH759240 KG00542-3
C 699	8.8	40.0	37	9	AA112840	AA112840 zns4f01.r	C 772	8.8	40.0	45	17	BH759240	BH759240 KG00542-3
C 700	8.8	40.0	37	9	AA112840	AA112840 zns4f01.r	C 773	8.8	40.0	46	17	BH759240	BH759240 KG00542-3
C 701	8.8	40.0	37	17	AZ814152	AZ814152 2M0081C13	C 774	8.8	40.0	46	9	AA837899	AA837899 0640d03.s
C 702	8.8	40.0	37	17	AZ814152	AZ814152 2M0081C13	C 775	8.8	40.0	46	9	AA837899	AA837899 0640d03.s
C 703	8.8	40.0	37	17	BH809857	BH809857 SALK_0064	C 776	8.8	40.0	46	9	AA540301	AA540301 t934d01.x
C 704	8.8	40.0	37	17	BH809857	BH809857 SALK_0064	C 777	8.8	40.0	46	9	AA540301	AA540301 t934d01.x
C 705	8.8	40.0	38	17	AZ439902	AZ439902 1M0230C13	C 778	8.8	40.0	46	9	AA543725	AA543725 vR26C08.r
C 706	8.8	40.0	38	17	AZ439902	AZ439902 1M0230C13	C 779	8.8	40.0	46	9	AA543725	AA543725 vR26C08.r
C 707	8.8	40.0	38	17	AZ772664	AZ772664 1M0583B16	C 780	8.8	40.0	46	14	D26039	D26039 HUMG003662
C 708	8.8	40.0	38	17	AZ772664	AZ772664 1M0583B16	C 781	8.8	40.0	46	14	D26039	D26039 HUMG003662
C 709	8.8	40.0	39	10	AV833438	AV833438 AV833438	C 782	8.8	40.0	46	14	T53599	T53599 y9a97f09.s1
C 710	8.8	40.0	39	10	AV833438	AV833438 AV833438	C 783	8.8	40.0	46	14	T53599	T53599 y9a97f09.s1
C 711	8.8	40.0	39	10	BE617821	BE617821 601441869	C 784	8.8	40.0	47	12	BG484978	BG484978 602503986
C 712	8.8	40.0	39	10	BE617821	BE617821 601441869	C 785	8.8	40.0	47	12	BG484978	BG484978 602503986
C 713	8.8	40.0	39	12	BF028281	BF028281 601765059	C 786	8.8	40.0	47	17	AZ476231	AZ476231 1M0294P14
C 714	8.8	40.0	39	12	BF028281	BF028281 601765059	C 787	8.8	40.0	47	17	AZ476231	AZ476231 1M0294P14
C 715	8.8	40.0	39	14	D26027	D26027 HUMG002394	C 788	8.8	40.0	47	17	AZ480070	AZ480070 1M0301K13
C 716	8.8	40.0	39	14	D26027	D26027 HUMG002394	C 789	8.8	40.0	47	17	AZ480070	AZ480070 1M0301K13
C 717	8.8	40.0	39	17	BH811645	BH811645 SALK_0595	C 790	8.8	40.0	47	17	BH636648	BH636648 1008012E0
C 718	8.8	40.0	39	17	BH811645	BH811645 SALK_0595	C 791	8.8	40.0	47	17	BH636648	BH636648 1008012E0
C 719	8.8	40.0	39	17	TA268H080	TA268H080	C 792	8.8	40.0	47	17	BH814821	BH814821 SALK_0671
C 720	8.8	40.0	39	17	TA268H080	TA268H080	C 793	8.8	40.0	48	17	AZ803589	AZ803589 2M0064N04
C 721	8.8	40.0	40	9	A1123628	A1123628 co15h04.x	C 794	8.8	40.0	48	17	AZ803589	AZ803589 2M0064N04
C 722	8.8	40.0	40	9	A1123628	A1123628 co15h04.x	C 795	8.8	40.0	49	9	A1808123	A1808123 wF53d07.x
C 723	8.8	40.0	40	9	AA529801	AA529801 vj12d07.r	C 796	8.8	40.0	49	9	A1808123	A1808123 wF53d07.x
C 724	8.8	40.0	40	9	AA529801	AA529801 vj12d07.r	C 797	8.8	40.0	49	9	BH130349	BH130349 G-6pJ3.f
C 725	8.8	40.0	42	9	AL677123	AL677123 AL677123	C 798	8.8	40.0	49	17	BH130349	BH130349 G-6pJ3.f
C 726	8.8	40.0	42	9	AL677123	AL677123 AL677123	C 799	8.8	40.0	50	9	AU102628	AU102628 AU102628
C 727	8.8	40.0	42	17	AZ777273	AZ777273 2M0011M04	C 800	8.8	40.0	50	9	AU102628	AU102628 AU102628
C 728	8.8	40.0	42	17	AZ777273	AZ777273 2M0011M04	C 801	8.8	40.0	50	9	AU102851	AU102851 AU102851
C 729	8.8	40.0	42	17	AZ805941	AZ805941 2M0067B07	C 802	8.8	40.0	50	9	AU102851	AU102851 AU102851
C 730	8.8	40.0	42	17	AZ805941	AZ805941 2M0067B07	C 803	8.8	40.0	50	9	AU103122	AU103122 AU103122
C 731	8.8	40.0	42	17	AZ867147	AZ867147 2M0177E21	C 804	8.8	40.0	50	9	AU103122	AU103122 AU103122
C 732	8.8	40.0	42	17	AZ867147	AZ867147 2M0177E21	C 805	8.8	40.0	50	9	AU103136	AU103136 AU103136
C 733	8.8	40.0	42	17	AL757728	AL757728 Arabidops	C 806	8.8	40.0	50	9	AU103136	AU103136 AU103136
C 734	8.8	40.0	43	17	AA878868	AA878868 cf88e01.s	C 807	8.8	40.0	50	9	AU103137	AU103137 AU103137
C 735	8.8	40.0	43	17	AA878868	AA878868 cf88e01.s	C 808	8.8	40.0	50	9	AU103137	AU103137 AU103137
C 736	8.8	40.0	43	9	AA878868	AA878868 cf88e01.s	C 809	8.8	40.0	50	9	AU103143	AU103143 AU103143

C 810	8.8	40.0	50	9	AU103143	AU103143	AU103143	883	8.6	39.1	36	17	AL771940	AL771940 Arabidops
C 811	8.8	40.0	50	9	AU103148	AU103148	AU103148	C 884	8.6	39.1	36	17	AL771940	AL771940 Arabidops
C 812	8.8	40.0	50	9	AU103148	AU103148	AU103148	C 885	8.6	39.1	36	17	TA345F060	TA345F060 T. brucei
C 813	8.8	40.0	50	9	AU103150	AU103150	AU103150	C 886	8.6	39.1	36	17	TA345F060	TA345F060 T. brucei
C 814	8.8	40.0	50	9	AU103150	AU103150	AU103150	C 887	8.6	39.1	37	9	AA007962	AA007962 mg66907.r
C 815	8.8	40.0	50	9	AU103828	AU103828	AU103828	C 888	8.6	39.1	37	9	AA007962	AA007962 mg66907.r
C 816	8.8	40.0	50	9	AU103828	AU103828	AU103828	C 889	8.6	39.1	37	9	AA889248	AA889248 ak26d11.s
C 817	8.8	40.0	50	9	AU104007	AU104007	AU104007	C 890	8.6	39.1	37	9	AA889248	AA889248 ak26d11.s
C 818	8.8	40.0	50	9	AU104007	AU104007	AU104007	C 891	8.6	39.1	37	9	AZ593655	AZ593655 1M040516
C 819	8.8	40.0	50	9	AU104105	AU104105	AU104105	C 892	8.6	39.1	37	17	AZ593655	AZ593655 1M040516
C 820	8.8	40.0	50	9	AU104105	AU104105	AU104105	C 893	8.6	39.1	37	17	AZ776442	AZ776442 2M0010L02
C 821	8.8	40.0	50	9	AU104120	AU104120	AU104120	C 894	8.6	39.1	37	17	AZ776442	AZ776442 2M0010L02
C 822	8.8	40.0	50	9	AU104120	AU104120	AU104120	C 895	8.6	39.1	37	17	AZ806718	AZ806718 2M0068024
C 823	8.8	40.0	50	9	AU104350	AU104350	AU104350	C 896	8.6	39.1	37	17	TA126E1P	TA126E1P
C 824	8.8	40.0	50	9	AU104350	AU104350	AU104350	C 897	8.6	39.1	37	17	TA126E1P	TA126E1P
C 825	8.8	40.0	50	9	AU104585	AU104585	AU104585	C 898	8.6	39.1	37	12	BF137365	BF137365
C 826	8.8	40.0	50	9	AU104585	AU104585	AU104585	C 899	8.6	39.1	38	12	BF137365	BF137365
C 827	8.8	40.0	50	9	AU104586	AU104586	AU104586	C 900	8.6	39.1	38	12	BF137365	BF137365
C 828	8.8	40.0	50	9	AU104586	AU104586	AU104586	C 901	8.6	39.1	38	13	BF137365	BF137365
C 829	8.8	40.0	50	9	AU104589	AU104589	AU104589	C 902	8.6	39.1	38	13	BF137365	BF137365
C 830	8.8	40.0	50	9	AU104589	AU104589	AU104589	C 903	8.6	39.1	38	13	BF137365	BF137365
C 831	8.8	40.0	50	9	AU105003	AU105003	AU105003	C 904	8.6	39.1	38	17	AL771951	AL771951 Arabidops
C 832	8.8	40.0	50	9	AU105003	AU105003	AU105003	C 905	8.6	39.1	39	17	AZ324421	AZ324421
C 833	8.8	40.0	50	9	AU105029	AU105029	AU105029	C 906	8.6	39.1	39	17	AZ324421	AZ324421
C 834	8.8	40.0	50	9	AU105029	AU105029	AU105029	C 907	8.6	39.1	39	17	AZ514516	AZ514516
C 835	8.8	40.0	50	9	AU105067	AU105067	AU105067	C 908	8.6	39.1	39	17	AZ514516	AZ514516
C 836	8.8	40.0	50	9	AU105067	AU105067	AU105067	C 909	8.6	39.1	40	17	AZ390083	AZ390083
C 837	8.8	40.0	50	9	AU105077	AU105077	AU105077	C 910	8.6	39.1	40	17	AZ390083	AZ390083
C 838	8.8	40.0	50	9	AU105077	AU105077	AU105077	C 911	8.6	39.1	40	17	AZ829500	AZ829500
C 839	8.8	40.0	50	9	AU105477	AU105477	AU105477	C 912	8.6	39.1	40	17	AZ829500	AZ829500
C 840	8.8	40.0	50	9	AU105477	AU105477	AU105477	C 913	8.6	39.1	41	13	BF148702	BF148702
C 841	8.8	40.0	50	9	AU105478	AU105478	AU105478	C 914	8.6	39.1	41	13	BF148702	BF148702
C 842	8.8	40.0	50	9	AU105478	AU105478	AU105478	C 915	8.6	39.1	41	17	BH637243	BH637243
C 843	8.8	40.0	50	9	AU105735	AU105735	AU105735	C 916	8.6	39.1	41	17	BH637243	BH637243
C 844	8.8	40.0	50	9	AU105735	AU105735	AU105735	C 917	8.6	39.1	42	14	D19980	D19980
C 845	8.8	40.0	50	9	AU105828	AU105828	AU105828	C 918	8.6	39.1	42	14	D19980	D19980
C 846	8.8	40.0	50	9	AU105828	AU105828	AU105828	C 919	8.6	39.1	43	9	A1084973	A1084973
C 847	8.8	40.0	50	9	AU105829	AU105829	AU105829	C 920	8.6	39.1	43	9	A1084973	A1084973
C 848	8.8	40.0	50	9	AU105829	AU105829	AU105829	C 921	8.6	39.1	43	9	A1789785	A1789785
C 849	8.8	40.0	50	9	AU105830	AU105830	AU105830	C 922	8.6	39.1	43	9	A1789785	A1789785
C 850	8.8	40.0	50	9	AU105830	AU105830	AU105830	C 923	8.6	39.1	43	9	A1790181	A1790181
C 851	8.8	40.0	50	9	AU105831	AU105831	AU105831	C 924	8.6	39.1	43	9	A1790181	A1790181
C 852	8.8	40.0	50	9	AU107008	AU107008	AU107008	C 925	8.6	39.1	43	9	AA499553	AA499553
C 853	8.8	40.0	50	9	AU107008	AU107008	AU107008	C 926	8.6	39.1	43	9	AA499553	AA499553
C 854	8.8	40.0	50	9	AU107008	AU107008	AU107008	C 927	8.6	39.1	44	17	CNS07R95	CNS07R95
C 855	8.8	40.0	50	9	AU107993	AU107993	AU107993	C 928	8.6	39.1	44	17	CNS07R95	CNS07R95
C 856	8.8	40.0	50	9	AU107993	AU107993	AU107993	C 929	8.6	39.1	45	13	BF190692	BF190692
C 857	8.8	40.0	50	12	BG148757	BG148757	BG148757	C 930	8.6	39.1	45	13	BF190692	BF190692
C 858	8.8	40.0	50	12	BG148757	BG148757	BG148757	C 931	8.6	39.1	45	13	BF190692	BF190692
C 859	8.8	40.0	50	12	BG569683	BG569683	BG569683	C 932	8.6	39.1	45	13	BF190692	BF190692
C 860	8.8	40.0	50	12	BG569683	BG569683	BG569683	C 933	8.6	39.1	45	13	BF190692	BF190692
C 861	8.8	40.0	50	17	AZ921856	AZ921856	AZ921856	C 934	8.6	39.1	45	17	AL753163	AL753163
C 862	8.8	40.0	50	17	AZ921856	AZ921856	AZ921856	C 935	8.6	39.1	45	17	AL753163	AL753163
C 863	8.8	40.0	25	17	AZ773296	AZ773296	AZ773296	C 936	8.6	39.1	48	17	TA372F02Q	TA372F02Q
C 864	8.6	39.1	25	17	AZ773296	AZ773296	AZ773296	C 937	8.6	39.1	48	17	TA372F02Q	TA372F02Q
C 865	8.6	39.1	27	14	D44905	D44905	D44905	C 938	8.6	39.1	49	9	AA123002	AA123002
C 866	8.6	39.1	27	14	D44905	D44905	D44905	C 939	8.6	39.1	49	9	AA123002	AA123002
C 867	8.6	39.1	28	9	A1020682	A1020682	A1020682	C 940	8.6	39.1	49	9	AA123002	AA123002
C 868	8.6	39.1	28	9	A1020682	A1020682	A1020682	C 941	8.6	39.1	49	9	AA123002	AA123002
C 869	8.6	39.1	30	17	AL752337	AL752337	AL752337	C 942	8.6	39.1	49	9	AA123002	AA123002
C 870	8.6	39.1	30	17	AL752337	AL752337	AL752337	C 943	8.6	39.1	49	9	AA123002	AA123002
C 871	8.6	39.1	31	9	A1522965	A1522965	A1522965	C 944	8.6	39.1	49	14	W99572	W99572
C 872	8.6	39.1	31	9	A1522965	A1522965	A1522965	C 945	8.6	39.1	50	9	W99572	W99572
C 873	8.6	39.1	31	14	U44252	U44252	U44252	C 946	8.6	39.1	50	9	W99572	W99572
C 874	8.6	39.1	31	14	U44252	U44252	U44252	C 947	8.6	39.1	50	9	W99572	W99572
C 875	8.6	39.1	31	17	AZ785865	AZ785865	AZ785865	C 948	8.6	39.1	50	9	W99572	W99572
C 876	8.6	39.1	31	17	AZ785865	AZ785865	AZ785865	C 949	8.6	39.1	50	9	W99572	W99572
C 877	8.6	39.1	33	17	AZ785865	AZ785865	AZ785865	C 950	8.6	39.1	50	9	W99572	W99572
C 878	8.6	39.1	33	17	AZ785865	AZ785865	AZ785865	C 951	8.6	39.1	50	9	W99572	W99572
C 879	8.6	39.1	34	17	AZ785865	AZ785865	AZ785865	C 952	8.6	39.1	50	9	W99572	W99572
C 880	8.6	39.1	34	9	AA500126	AA500126	AA500126	C 953	8.6	39.1	50	9	W99572	W99572
C 881	8.6	39.1	34	17	TA327F04Q	TA327F04Q	TA327F04Q	C 954	8.6	39.1	50	9	W99572	W99572
C 882	8.6	39.1	34	17	TA327F04Q	TA327F04Q	TA327F04Q	C 955	8.6	39.1	50	9	W99572	W99572

C 956	8.6	39.1	50	9	AU104348	AU104348
C 957	8.6	39.1	50	9	AU105911	AU105911
C 958	8.6	39.1	50	9	AU105911	AU105911
C 959	8.6	39.1	50	9	AU106266	AU106266
C 960	8.6	39.1	50	9	AU106266	AU106266
C 961	8.6	39.1	50	9	AU106809	AU106809
C 962	8.6	39.1	50	9	AU106809	AU106809
C 963	8.6	39.1	50	9	AU106810	AU106810
C 964	8.6	39.1	50	9	AU106810	AU106810
C 965	8.6	39.1	50	9	AU106811	AU106811
C 966	8.6	39.1	50	9	AU106811	AU106811
C 967	8.6	39.1	50	9	AU106812	AU106812
C 968	8.6	39.1	50	9	AU106812	AU106812
C 969	8.6	39.1	50	9	AU106813	AU106813
C 970	8.6	39.1	50	9	AU106813	AU106813
C 971	8.6	39.1	50	9	AU106814	AU106814
C 972	8.6	39.1	50	9	AU106814	AU106814
C 973	8.6	39.1	50	9	AU106815	AU106815
C 974	8.6	39.1	50	9	AU106815	AU106815
C 975	8.6	39.1	50	9	AU106816	AU106816
C 976	8.6	39.1	50	9	AU106816	AU106816
C 977	8.6	39.1	50	9	AU106817	AU106817
C 978	8.6	39.1	50	9	AU106817	AU106817
C 979	8.6	39.1	50	9	AU106818	AU106818
C 980	8.6	39.1	50	9	AU106818	AU106818
C 981	8.6	39.1	50	9	AU106819	AU106819
C 982	8.6	39.1	50	9	AU106819	AU106819
C 983	8.6	39.1	50	9	AU106820	AU106820
C 984	8.6	39.1	50	9	AU106820	AU106820
C 985	8.6	39.1	50	9	AU106821	AU106821
C 986	8.6	39.1	50	9	AU106821	AU106821
C 987	8.6	39.1	50	9	AU106822	AU106822
C 988	8.6	39.1	50	9	AU106822	AU106822
C 989	8.6	39.1	50	9	AU107694	AU107694
C 990	8.6	39.1	50	9	AU107694	AU107694
C 991	8.6	39.1	50	9	AU107978	AU107978
C 992	8.6	39.1	50	9	AU107978	AU107978
C 993	8.6	39.1	50	10	AV956714	AV956714
C 994	8.6	39.1	50	10	AV956714	AV956714
C 995	8.6	39.1	50	17	BH790247	BH790247
C 996	8.6	39.1	50	17	BH790247	BH790247
C 997	8.4	38.2	22	17	AZ342067	AZ342067
C 998	8.4	38.2	22	17	HSMC03F05	HSMC03F05
C 999	8.4	38.2	23	17	HSMC03F05	HSMC03F05
C1000	8.4	38.2	23	17	HSMC03F05	HSMC03F05

ALIGNMENTS

RESULT 1
A1749566 48 bp mRNA linear EST 22-JUN-1999
LOCUS A330101.x1 Bartshead colon HPLRB7 Homo sapiens cDNA clone
DEFINITION IMAGE:2373529 3' similar to SW:RS29_HUMAN P30054 40S RIBOSOMAL
PROTEIN S29. ; mRNA sequence.
A1749566
ACCESSION A1749566.1 GI:5127830
VERSION EST.
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 48)
AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
Kizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Maira, M., Martin,
J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B.,
White, Y., Wylie, T., Waterston, R. and Wilson, R.
TITLE Washu-NCI human EST project
JOURNAL Unpublished (1997)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

FEATURES
Source
1. 48
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2373529"
/clone_1b="Bartshead colon HPLRB7"
/sex="male"
/dev_stage="adult, age 25"
/lab_host="DH10B (phage resistant)"
/note="Organ: colon; Vector: pT73D-pac (Pharmacia) with a
modified polylinker; Site 1: EcoRI; Site 2: NotI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer (5'
3'), double-stranded cDNA was ligated to Eco RI adaptors
15' AATCAGTAAAT 3' and 5' ATTACTAGTG 3', digested
with Not I and cloned into the Not I and Eco RI sites of
the modified pT73 vector. Library constructed by Bob
Bartshead."

BASE COUNT 15 a 14 c 9 g 10 t
ORIGIN

Query Match 57.3%; Score 12.6; DB 9; Length 48;
Best Local Similarity 78.9%; Pred. No. 5.4e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

CY 2 TGAGCCGATATCGCTTC 20
10 TGAACCGATATCTTCGC 28
Db

RESULT 2
A1749566/c 48 bp mRNA linear EST 22-JUN-1999
LOCUS A330101.x1 Bartshead colon HPLRB7 Homo sapiens cDNA clone
DEFINITION IMAGE:2373529 3' similar to SW:RS29_HUMAN P30054 40S RIBOSOMAL
PROTEIN S29. ; mRNA sequence.
A1749566
ACCESSION A1749566.1 GI:5127830
VERSION EST.
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 48)
AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
Kizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Maira, M., Martin,
J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B.,
White, Y., Wylie, T., Waterston, R. and Wilson, R.
TITLE Washu-NCI human EST project
JOURNAL Unpublished (1997)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone; similarity on wrong strand
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers 1. 48

FEATURES
source 1. 48

QY	1	CTGAGACGATATCGCTTCAG	22			1
----	---	----------------------	----	--	--	---

DB	24	CTGAGACCGTGGCGGTCTGTG	45
RESULT 4			
LOCUS	AUI03408/c	50 bp	mRNA linear
DEFINITION	AUI03408 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone		EST 30-AUG-2001
ACCESSION	HEB00818, mRNA sequence.		
VERSION	AUI03408		
KEYWORDS	AUI03408.1 GI:13552929		
SOURCE	EST.		
ORGANISM	human.		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	1 (bases 1 to 50)		
JOURNAL	Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata		
MEDLINE	'H., Ota, T., Isega, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki		
COMMENT	Y., Nakamura, Y., Suyama, A. and Sugano, S. Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites		
	EMBO Rep. 2 (5), 388-393 (2001)		
	21270072		
	Contact: Yutaka Suzuki:		
	Department of Virology		
	Institute of Medical Science, University of Tokyo		
	4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan		
	Email: yasuaki@ims.u-tokyo.ac.jp		
	Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano		
	S., Construction and characterization of a full length-enriched and		
	a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).		
FEATURES	Location/Qualifiers		
source	1..50		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone="HEB00818"		
	/clone_lib="Sugano Homo sapiens cDNA library"		
	/note="Differential display comparison of untreated and		
	dimethylfumarate treated u937 cells"		
BASE COUNT	3 a 21 c 14 g 12 t.		
ORIGIN			
Query Match	56.4%; Score 12.4; DB 9; Length 50;		
Best Local Similarity	72.7%; Pred. No. 6.8e+04;		
Matches	16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;		
QY	1 CTGAGACCGATATGCGTCTGAG 22		
Db	45 CAGAGACCGCCGACGGTCTGTG 24		
RESULT 5			
LOCUS	AZ511046	32 bp	DNA linear
DEFINITION	IM0355120R Mouse 10kb plasmid UUGC1M library Mus musculus genomic		
ACCESSION	clone UUGC1M0355120 R, DNA sequence.		
VERSION	AZ511046		
KEYWORDS	AZ511046.1 GI:10692362		
SOURCE	GSS.		
ORGANISM	house mouse.		
	Mus musculus		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
REFERENCE	1 (bases 1 to 32)		
AUTHORS	Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C.,		
	Islam, H., Longacre, S., Mamoud, M., Meenen, E., Pedersen, T., Reilly		
	, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.		
	and Wright, D., Weis, R.		
	Mouse whole genome scaffolding with paired end reads from 10kb		
	plasmid inserts		
	Unpublished (2000)		
JOURNAL	Contact: Robert B. Weiss		
COMMENT	University of Utah Genome Center		

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0355 row: 1 column: 20
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 32.
Location/Qualifiers
1. .32

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0355120"
/clone_id="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g14732114[gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT

14 a 4 c 3 g 11 t

ORIGIN

Query Match 54.5%; Score 12; DB 17; Length 32;
Best Local Similarity 75.0%; Pred. No. 9.2e+04;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 2 TGAGACCGATTCGCTCA 21
|||||
|||||

Db 6 TAAGACATATTAAGTCTCA 25
|||||
|||||

RESULT 6

AZ511046/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

JOURNAL

COMMENT

32 bp DNA linear GSS 05-OCT-2000
1M0355120R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0355120 R, DNA sequence.

AZ511046.1 GI:10692362

GSS.

house mouse.

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murineae; Mus.

1 (bases 1 to 32)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,

M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.

and Wright, D., Weis, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weis

University of Utah Genome Center

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0355 row: 1 column: 20
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 32.
Location/Qualifiers
1. .32

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0355120"
/clone_id="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g14732114[gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT

14 a 4 c 3 g 11 t

ORIGIN

Query Match 54.5%; Score 12; DB 17; Length 32;
Best Local Similarity 75.0%; Pred. No. 9.2e+04;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 2 TGAGACCGATTCGCTCA 21
|||||
|||||

Db 25 TGAGACTTATATATGCTTA 6
|||||
|||||

RESULT 7

N32567

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

JOURNAL

COMMENT

37 bp mRNA linear EST 10-JAN-1996
YW86605.s1 Soares placenta 809weeks 2NbHP809W Homo sapiens CDNA
clone IMAGE:259136.3' similar to gb:X52192 PROTO-ONCOGENE
TYROSINE-PROTEIN KINASE FES/FPS (HUMAN);, mRNA sequence.

N32567.1 GI:1152966

EST.

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 37)

Hillier, L., Clark, N., Dubuque, T., Eliston, K., Hawkins, M., Holman

M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marita, M., Parsons, J.,

Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevisakis, E., Waterston

R., Williamson, A., Wohlmann, P., and Wilson, R.

The Washu-Merck EST Project

Unpublished (1995)

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 High quality sequence starts: 1
 Source: IMAGE Consortium, LNL
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 Trace considered overall poor quality
 Seq primer: m13 -40 forward
 High quality sequence stop: 1.

FEATURES

source

1. .37
 /organism="Homo sapiens"
 /db_xref="GDB:388842"
 /db_xref="taxon:9606"
 /clone="IMAGE:259136"
 /clone_lib="Soares_placenta_8to9weeks_2NBHP8to9W"
 /dev_stage="two placentae: one from 8 weeks and another
 from 9 weeks post conception"
 /lab_host="DH10B (ampicillin resistant)"
 /note="Organ: placenta; Vector: p773D (Pharmacia) with a
 modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
 strand cDNA was primed with a Not I - oligo (dt) primer [5'
 TGTACCAATCTGAAGTGGAGCGCGCATTTTCTTTTCTTTT 3']
 double-stranded cDNA was size selected, ligated to Eco RI
 adapters (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of a modified p773 vector
 (Pharmacia). Library constructed by Bento Soares and
 M. Fatima Bonaldo."

BASE COUNT

5 a 10 c 11 g 10 t 1 others

ORIGIN

Query Match 54.5%; Score 12; DB 14; Length 37;
 Best Local Similarity 71.4%; Pred. No. 9.6e+04;
 Matches 15; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Y

1 CTGAGACCGATATCGGTCTCA 21

Db

14 CTGATGCCGNTTTCAGCTCA 34

RESULT 8
 N32567/c 37 bp mRNA linear EST 10-JAN-1996
 LOCUS
 DEFINITION
 N32567.yw86e05.s1 Soares_placenta_8to9weeks_2NBHP8to9W Homo sapiens CDNA
 clone IMAGE:259136 3' similar to gb:X52192 PROTO-ONCOGENE
 TYROSINE-PROTEIN KINASE FES/FPS (HUMAN); mRNA sequence.

VERSION
 N32567
 EST.
 N32567.1 GI:1152966

SOURCE

human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 37)
 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman
 'M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J.,
 Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston
 'R., Williamson, A., Wohlmann, P. and Wilson, R.
 The WashU-Merck EST Project
 Unpublished (1995)

TITLE

JOURNAL

COMMENT

Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 High quality sequence starts: 1
 High quality sequence stops: 1
 Source: IMAGE Consortium, LNL
 This clone is available royalty-free through LNL; contact the

IMAGE Consortium (info@image.lnl.gov) for further information.
 Trace considered overall poor quality
 Seq primer: m13 -40 forward
 High quality sequence stop: 1.

FEATURES

source

1. .37
 /organism="Homo sapiens"
 /db_xref="GDB:388842"
 /db_xref="taxon:9606"
 /clone="IMAGE:259136"
 /clone_lib="Soares_placenta_8to9weeks_2NBHP8to9W"
 /dev_stage="two placentae: one from 8 weeks and another
 from 9 weeks post conception"
 /lab_host="DH10B (ampicillin resistant)"
 /note="Organ: placenta; Vector: p773D (Pharmacia) with a
 modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
 strand cDNA was primed with a Not I - oligo (dt) primer [5'
 TGTACCAATCTGAAGTGGAGCGCGCATTTTCTTTTCTTTT 3']
 double-stranded cDNA was size selected, ligated to Eco RI
 adapters (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of a modified p773 vector
 (Pharmacia). Library constructed by Bento Soares and
 M. Fatima Bonaldo."

BASE COUNT

5 a 10 c 11 g 10 t 1 others

ORIGIN

Query Match 54.5%; Score 12; DB 14; Length 37;
 Best Local Similarity 71.4%; Pred. No. 9.6e+04;
 Matches 15; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Y

2 TGAGACCGATATCGGTCTCAG 22

Db

34 TGAGCTGAANCGCATCAG 14

RESULT 9
 B1769009 39 bp mRNA linear EST 25-SEP-2001
 LOCUS
 DEFINITION
 B1769009.603058167F1 NIH_MGC_122 Homo sapiens CDNA clone IMAGE:5207441 5',
 mRNA sequence.

VERSION
 B1769009
 EST.
 B1769009.1 GI:15760587

SOURCE

human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 39)
 NIH-MGC http://imgc.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

JOURNAL

COMMENT

DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.lnl.gov
 Plate: LLM41520 row: f column: 18
 High quality sequence stop: 39.

FEATURES

source

1. .39
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5207441"
 /clone_lib="NIH_MGC_122"
 /lab_host="DH10B"
 /note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
 Site_1: NotI; Site_2: EcoRV (destroyed); RNA source
 anonymous pool of 24 week female lung, 16 week female
 spleen, and 20-22 week male spleens. Library is oligo-dT

primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note: this is a NIH MGC Library."

BASE COUNT 3 a 9 c 20 g 7 t

Query Match 54.5%; Score 12; DB 13; Length 39;

Best Local Similarity 75.0%; Pred. NO. 9.7e+04; Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CTGAGACCATATCGCTCTC 20
12 CTGCGACTGCTGCTGCTC 31

RESULT 10
B1769009/c 39 bp mRNA linear EST 25-SEP-2001
LOCUS 603058167F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5207441 5',
DEFINITION mRNA sequence.

ACCESSION B1769009
VERSION B1769009.1 GI:15760587
KEYWORDS EST:
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 39)
AUTHORS NIH-MGC http://mgs.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at:
http://image.lnl.gov
Plate: L1AM1520 row: F column: 18
High quality sequence stop: 39.

FEATURES
source location/Qualifiers
1..39

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5207441"
/clone_1ib="NIH MGC_122"
/lab_host="MDH10B"
/note="Organ: pooled lung and spleen. Vector: pCMV-SportE; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dt primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note: this is a NIH MGC Library."
BASE COUNT 3 a 9 c 20 g 7 t

Query Match 54.5%; Score 12; DB 13; Length 39;
Best Local Similarity 75.0%; Pred. NO. 9.7e+04;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 GAGACCATATCGCTCTCAG 22
31 GACACCGACGACGCTCGCAG 12

RESULT 11
AUI06749 50 bp mRNA linear EST 30-AUG-2001
LOCUS AUI06749 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION RAT05789, mRNA sequence.

ACCESSION AUI06749
VERSION AUI06749.1 GI:13556270
KEYWORDS EST:
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 50)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

TITLE Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
JOURNAL 21270072
MEDLINE
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshimoto-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
Location/Qualifiers

FEATURES
source 1..50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="KAT05789"
/clone_1ib="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and dimethylsulphate treated U937 cells"

BASE COUNT 8 a 11 c 18 g 13 t

Query Match 54.5%; Score 12; DB 9; Length 50;
Best Local Similarity 75.0%; Pred. NO. 1e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 GAGACCATATCGCTCTCAG 22
5 GAGACCGATAGCTGCTTCG 24

RESULT 12
AUI06749 50 bp mRNA linear EST 30-AUG-2001
LOCUS AUI06749 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION RAT05789, mRNA sequence.

ACCESSION AUI06749
VERSION AUI06749.1 GI:13556270
KEYWORDS EST:
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 50)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

TITLE Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
JOURNAL 21270072
MEDLINE
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: yusuzuki@ims.u-tokyo.ac.jp
 Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano
 S. Construction and characterization of a full length-enriched and
 a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES

Source

1. 50
 /organism="Homo sapiens"
 /db xref="taxon:9606"
 /clone.lib="Sugano Homo sapiens cDNA library"
 /note="Differential display comparison of untreated and
 dimethylitumarate treated U937 cells"
 8 a 11 c 18 g 13 t

BASE COUNT

ORIGIN

Query Match 54.5%; Score 12; DB 9; Length 50;
 Best Local Similarity 75.0%; Pred. No. 1e+05; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 5;

Qy 1 CTGAGACCGATATCGTCTC 20
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 Db 24 CCGAGACGCTATCGTCTC 5

RESULT 13
 AUI07183 50 bp mRNA linear EST 30-AUG-2001
 LOCUS AUI07183 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
 DEFINITION COLF0623, mRNA sequence.

ACCESSION AUI07183
 VERSION AUI07183.1 GI:13556704
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 50)
 Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata
 H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki
 Y., Nakamura, Y., Suyama, A. and Sugano, S.
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 S. Construction and characterization of a full length-enriched and
 a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES

Source

1. 50
 /organism="Homo sapiens"
 /db xref="taxon:9606"
 /clone.lib="Sugano Homo sapiens cDNA library"
 /note="Differential display comparison of untreated and
 dimethylitumarate treated U937 cells"
 10 a 13 c 14 g 13 t

BASE COUNT

ORIGIN

Query Match 54.5%; Score 12; DB 9; Length 50;
 Best Local Similarity 75.0%; Pred. No. 1e+05; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 5;

Qy 1 CTGAGACCGATATCGTCTC 20
 |||||
 Db 20 CTGAGACGCTATCGTCTC 39

RESULT 14

AUI07183/c 50 bp mRNA linear EST 30-AUG-2001
 LOCUS AUI07183 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
 DEFINITION COLF0623, mRNA sequence.

ACCESSION AUI07183
 VERSION AUI07183.1 GI:13556704
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 50)
 Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata
 H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki
 Y., Nakamura, Y., Suyama, A. and Sugano, S.
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 S. Construction and characterization of a full length-enriched and
 a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES

Source

1. 50
 /organism="Homo sapiens"
 /db xref="taxon:9606"
 /clone.lib="Sugano Homo sapiens cDNA library"
 /note="Differential display comparison of untreated and
 dimethylitumarate treated U937 cells"
 10 a 13 c 14 g 13 t

BASE COUNT

ORIGIN

Query Match 54.5%; Score 12; DB 9; Length 50;
 Best Local Similarity 75.0%; Pred. No. 1e+05; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 5;

Qy 3 GAGACCGATATCGTCTCAG 22
 |||||
 Db 39 GTGACCCATCTGCTCTCAG 20

RESULT 15
 AUI07184 50 bp mRNA linear EST 30-AUG-2001
 LOCUS AUI07184 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
 DEFINITION COLF1135, mRNA sequence.

ACCESSION AUI07184
 VERSION AUI07184.1 GI:13556705
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 50)
 Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata
 H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki
 Y., Nakamura, Y., Suyama, A. and Sugano, S.
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Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano

.S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
source
1..50
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/db_xref="taxon:9606"
/clone="COLF1135"
/note="Differential display comparison of untreated and dimethylfumarate treated U937 cells"

BASE COUNT
11 a 13 c 13 g 13 t

ORIGIN
Query Match 54.5%; Score 12; DB 9; Length 50;
Best Local Similarity 75.0%; Pred. No. 1e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CTGAGCCGATATCGTCTC 20
|||||
20 CTGAGACGACGATGCTCAC 39

RESULT 16
AUI07184 50 bp mRNA linear EST 30-AUG-2001
LOCUS AUI07184 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION COLF1135, mRNA sequence.
ACCESSION AUI07184
VERSION AUI07184.1 GI:13556705
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata ,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki ,Y., Nakamura,Y., Suyama,A. and Sugano,S.
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TITLE mapping of mRNA start sites

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COMMENT Contact: Yutaka Suzuki
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Email: yusuzuki@ims.u-tokyo.ac.jp

FEATURES
source
1..50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="COLF1135"
/note="Differential display comparison of untreated and dimethylfumarate treated U937 cells"

BASE COUNT
11 a 13 c 13 g 13 t

ORIGIN
Query Match 54.5%; Score 12; DB 9; Length 50;
Best Local Similarity 75.0%; Pred. No. 1e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 GAGACCGATATCGTCTCAG 22
|||||
39 GTGACCGATCTTGCTCAG 20

RESULT 17
AUI07185 50 bp mRNA linear EST 30-AUG-2001
LOCUS AUI07185 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION COLF1135, mRNA sequence.
ACCESSION AUI07185
VERSION AUI07185.1 GI:13556706
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata ,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki ,Y., Nakamura,Y., Suyama,A. and Sugano,S.
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TITLE mapping of mRNA start sites

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COMMENT Contact: Yutaka Suzuki
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Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp

FEATURES
source
1..50
/organism="Homo sapiens"
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/clone="HEP02932"
/note="Differential display comparison of untreated and dimethylfumarate treated U937 cells"

BASE COUNT
11 a 13 c 13 g 13 t

ORIGIN
Query Match 54.5%; Score 12; DB 9; Length 50;
Best Local Similarity 75.0%; Pred. No. 1e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CTGAGCCGATATCGTCTC 20
|||||
21 CTGAGACGACGATGCTCAC 40

RESULT 18
AUI07185 50 bp mRNA linear EST 30-AUG-2001
LOCUS AUI07185 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION HEP02932, mRNA sequence.
ACCESSION AUI07185
VERSION AUI07185.1 GI:13556706
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata ,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki ,Y., Nakamura,Y., Suyama,A. and Sugano,S.
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4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp

FEATURES
source
1..50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HEP02932"
/note="Differential display comparison of untreated and dimethylfumarate treated U937 cells"

BASE COUNT
11 a 13 c 13 g 13 t

ORIGIN
Query Match 54.5%; Score 12; DB 9; Length 50;
Best Local Similarity 75.0%; Pred. No. 1e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CTGAGCCGATATCGTCTC 20
|||||
21 CTGAGACGACGATGCTCAC 40

AUI07185 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HEP02932, mRNA sequence.
AUI07185
VERSION AUI07185.1 GI:13556706
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata ,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki ,Y., Nakamura,Y., Suyama,A. and Sugano,S.
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Email: yusuzuki@ims.u-tokyo.ac.jp

FEATURES
source
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/db_xref="taxon:9606"
/clone="HEP02932"
/note="Differential display comparison of untreated and dimethylfumarate treated U937 cells"

BASE COUNT
11 a 13 c 13 g 13 t

ORIGIN
Query Match 54.5%; Score 12; DB 9; Length 50;
Best Local Similarity 75.0%; Pred. No. 1e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CTGAGCCGATATCGTCTC 20
|||||
21 CTGAGACGACGATGCTCAC 40

RESULT 18
AUI07185 50 bp mRNA linear EST 30-AUG-2001
LOCUS AUI07185 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION HEP02932, mRNA sequence.
ACCESSION AUI07185
VERSION AUI07185.1 GI:13556706
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata ,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki ,Y., Nakamura,Y., Suyama,A. and Sugano,S.
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TITLE mapping of mRNA start sites

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4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp

FEATURES
source
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HEP02932"
/note="Differential display comparison of untreated and dimethylfumarate treated U937 cells"

BASE COUNT
11 a 13 c 13 g 13 t

ORIGIN
Query Match 54.5%; Score 12; DB 9; Length 50;
Best Local Similarity 75.0%; Pred. No. 1e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CTGAGCCGATATCGTCTC 20
|||||
21 CTGAGACGACGATGCTCAC 40

FEATURES
source
Location/Qualifiers
1. .50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HEP02932"
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/note="Differential display comparison of untreated and dimethylflumarate treated U937 cells"

BASE COUNT
11 a 13 c 13 g 13 t

Query Match 54.5%; Score 12; DB 9; Length 50;
Best Local Similarity 75.0%; Pred. No. 1e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 GAGACCGATTCGCTCAG 22
Db 40 GTACCCATCTGCTCTCAG 21

RESULT 19
LOCUS AU107188 50 bp mRNA linear EST 30-AUG-2001
DEFINITION AU107188 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
ACCESSION AU107188
VERSION AU107188
KEYWORDS mRNA sequence.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
TITLE Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
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Location/Qualifiers

FEATURES
source
1. .50
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/db_xref="taxon:9606"
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/note="Differential display comparison of untreated and dimethylflumarate treated U937 cells"

BASE COUNT
10 a 14 c 11 g 15 t

Query Match 54.5%; Score 12; DB 9; Length 50;
Best Local Similarity 75.0%; Pred. No. 1e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CTGAGACCGATTCGCTC 20
Db 26 CTGAGAGCAAGATGGTCAC 45

RESULT 20
LOCUS AU107188 50 bp mRNA linear EST 30-AUG-2001
DEFINITION AU107188 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
ACCESSION AU107188
VERSION AU107188
KEYWORDS mRNA sequence.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

ACCESSION AU107188
VERSION AU107188.1 GI:13556709
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
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JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
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COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
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Location/Qualifiers

FEATURES
source
1. .50
/organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone_lib="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and dimethylflumarate treated U937 cells"

BASE COUNT
10 a 14 c 11 g 15 t

Query Match 54.5%; Score 12; DB 9; Length 50;
Best Local Similarity 75.0%; Pred. No. 1e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 GAGACCGATTCGCTCAG 22
Db 45 GTACCCATCTGCTCTCAG 26

RESULT 21
LOCUS AU107189 50 bp mRNA linear EST 30-AUG-2001
DEFINITION AU107189 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
ACCESSION AU107189
VERSION AU107189
KEYWORDS mRNA sequence.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
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MEDLINE 21270072
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Department of Virology
Institute of Medical Science, University of Tokyo
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Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
Location/Qualifiers

FEATURES
source
1. .50

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/db_xref="taxon:9606"
/clone="KAI1A4023"
/clone_lib="Sugano Homo sapiens cDNA library"
/notes="Differential display comparison of untreated and
dimethylfluminate treated U937 cells"
BASE COUNT      10 a      12 c      13 g      15 t
ORIGIN
Query Match      54.5%; Score 12; DB 9; Length 50;
Best Local Similarity 75.0%; Pred. No. 1e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
OY      1 CTGAGCCGATATCGTCTC 20
      22 CTGAGCCGATATCGTCTC 41
Db

RESULT 22
AUI07189/c      50 bp      mRNA      linear      EST 30-AUG-2001
LOCUS
DEFINITION      AUI07189 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
KAI1A4023, mRNA sequence.
ACCESSION      AUI07189
VERSION
KEYWORDS
SOURCE
ORGANISM
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tanoda,T., Mizushima-Sugano,J., Sese,J., Hara
,H., Ota,T., Isegaki,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
,Y., Nakamura,Y., Suyama,A. and Sugano,S.
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Email: yusuzuki@ims.u-tokyo.ac.jp
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,S.
Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES
SOURCE
1..50
/organism="Homo sapiens"
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/clone="KAI1A4023"
/clone_lib="Sugano Homo sapiens cDNA library"
/notes="Differential display comparison of untreated and
dimethylfluminate treated U937 cells"
BASE COUNT      10 a      12 c      13 g      15 t
ORIGIN
Query Match      54.5%; Score 12; DB 9; Length 50;
Best Local Similarity 75.0%; Pred. No. 1e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
OY      3 GAGACCGATATCGTCTCAG 22
      41 GTGACCATCTTGTCTCTCAG 22
Db

RESULT 23
AUI013431      32 bp      mRNA      linear      EST 03-AUG-1998
LOCUS
DEFINITION      AUI013431 Schizosaccharomyces pombe late log phase cDNA
Schizosaccharomyces pombe cDNA clone spc08150, mRNA sequence.
ACCESSION      AUI013431
VERSION
KEYWORDS
SOURCE
ORGANISM
AUI013431.1 GI:3368222

```

```

KEYWORDS
SOURCE
ORGANISM
Schizosaccharomyces pombe
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
REFERENCE
1 (bases 1 to 32)
Moriyomo,M. and Mita,K.
Identification of expressed sequence tags of Schizosaccharomyces
pombe
Unpublished (1998)
Contact: Mitsuo Moriyo
Genome Research Group
National Institute of Radiological Sciences
9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
Email: moriyomo@nirs.go.jp.
FEATURES
SOURCE
1..32
/organism="Schizosaccharomyces pombe"
/strain="972"
/db_xref="taxon:4896"
/clone="spc08150"
/clone_lib="Schizosaccharomyces pombe late log phase cDNA"
/sex="h minus"
/notes="Vector: M13mp19, The cDNA library of
Schizosaccharomyces pombe was prepared by cloning cDNA
into the SmaI site of M13mp19 DNA and the direction of DNA
sequences was not always from 5' to 3'. The cDNA data of
Schizosaccharomyces pombe are available for searching on
the World Wide Web. (URL: http://www.nirs.go.jp)"
BASE COUNT      11 a      5 c      11 g      4 t
ORIGIN
Query Match      53.6%; Score 11.8; DB 9; Length 32;
Best Local Similarity 81.2%; Pred. No. 1.1e+05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY      3 GAGACCGATATCGTCTC 18
      3 GAGACCGATATCGTCTC 18
Db

RESULT 24
AUI013431/c      32 bp      mRNA      linear      EST 03-AUG-1998
LOCUS
DEFINITION      AUI013431 Schizosaccharomyces pombe late log phase cDNA
Schizosaccharomyces pombe cDNA clone spc08150, mRNA sequence.
ACCESSION      AUI013431
VERSION
KEYWORDS
SOURCE
ORGANISM
Schizosaccharomyces pombe
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
1 (bases 1 to 32)
Moriyomo,M. and Mita,K.
Identification of expressed sequence tags of Schizosaccharomyces
pombe
Unpublished (1998)
Contact: Mitsuo Moriyo
Genome Research Group
National Institute of Radiological Sciences
9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
Email: moriyomo@nirs.go.jp.
FEATURES
SOURCE
1..32
/organism="Schizosaccharomyces pombe"
/strain="972"
/db_xref="taxon:4896"
/clone="spc08150"
/clone_lib="Schizosaccharomyces pombe late log phase cDNA"
/sex="h minus"

```

/note="Vector: M13mp19; The cDNA library of Schizosaccharomyces pombe was prepared by cloning cDNA into the SmaI site of M13mp19 DNA and the direction of DNA sequences was not always from 5' to 3'. The cDNA data of Schizosaccharomyces pombe are available for searching on the World Wide Web. (URL, <http://www.nirs.go.jp>)"

BASE COUNT 11 a 5 c 11 g 4 t 1 others

ORIGIN

Query Match 53.6%; Score 11.8; DB 9; Length 32;
Best Local Similarity 81.2%; Pred. No. 1.1e+05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 GACCGATATCGTCTC 20
18 GTNCGCTATCGTCTC 3

Db

RESULT 25 42 bp DNA linear GSS 25-APR-2002
BH805089 1008065D09.1EL_Y1 1008 - RescueMu Grid I Zea mays genomic, DNA
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

53.6%; Score 11.8; DB 9; Length 32;
Pred. No. 1.1e+05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1008065D09.1EL_Y1 1008 - RescueMu Grid I Zea mays genomic, DNA

BH805089
BH805089
BH805089.1 GI:20322013
GSS.
Zea mays.
Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 42)
Walbot, V.
Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
Contact: Walbot, V.
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Very probable ligation site of ends cut by single endonuclease.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1008065 column: 23
Class: transposon-tagged.
Location/Qualifiers
1. 42
/organism="Zea mays"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/clone_lib="1008 - RescueMu Grid I"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: leaf; Vector: RescueMu (engineered from pBluescript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site www.zmbl.iaslate.edu and follow the links for 'RescueMu'. Grid I was grown at Berkeley in 2001. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

BASE COUNT 11 a 13 c 9 g 9 t

ORIGIN

Query Match 53.6%; Score 11.8; DB 17; Length 42;
Best Local Similarity 86.7%; Pred. No. 1.2e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY

RESULT 27 43 bp DNA linear GSS 29-SEP-2000
AZ304932 1M0005G03F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
LOCUS
DEFINITION
ACCESSION

QY 7 CCGATATCGTCTCA 21
19 CCGATCTCGTCTCA 33

Db

RESULT 26 42 bp DNA linear GSS 25-APR-2002
BH805089 1008065D09.1EL_Y1 1008 - RescueMu Grid I Zea mays genomic, DNA
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

53.6%; Score 11.8; DB 17; Length 42;
Pred. No. 1.2e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1008065D09.1EL_Y1 1008 - RescueMu Grid I Zea mays genomic, DNA

BH805089
BH805089
BH805089.1 GI:20322013
GSS.
Zea mays.
Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 42)
Walbot, V.
Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
Contact: Walbot, V.
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Very probable ligation site of ends cut by single endonuclease.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1008065 column: 23
Class: transposon-tagged.
Location/Qualifiers
1. 42
/organism="Zea mays"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/clone_lib="1008 - RescueMu Grid I"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: leaf; Vector: RescueMu (engineered from pBluescript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site www.zmbl.iaslate.edu and follow the links for 'RescueMu'. Grid I was grown at Berkeley in 2001. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

BASE COUNT 11 a 13 c 9 g 9 t

ORIGIN

Query Match 53.6%; Score 11.8; DB 17; Length 42;
Best Local Similarity 86.7%; Pred. No. 1.2e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGAGACGATATCGG 16
33 TGAGACGAGATCGG 19

Db

RESULT 27 43 bp DNA linear GSS 29-SEP-2000
AZ304932 1M0005G03F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
LOCUS
DEFINITION
ACCESSION

VERSION	AZ304932.1	GI:10341444
KEYWORDS	GSS.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scuriognathi; Muridae; Murinae; Mus. 1 (bases 1 to 43)	
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Baconn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.	
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts	
JOURNAL	Unpublished (2000)	
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: dunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0005 row: G column: 03 Seq primer: CGTGTAAACGACGCGCAGT Class: plasmid cont High quality sequence stop: 43. Location/Qualifiers 1..43	
FEATURES		
SOURCE		

BASE COUNT
13 a 9 c 9 g 12 t

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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="tUGC1M0005G03"
/clone_lib="Mouse 10kb plasmid tUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g14732114[gB]/AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```

Query Match	53.6%	Score 11.8	DB 17	Length 43
Best Local Similarity	86.7%	Pred. No. 1.2e+05		
Matches 13, Conservative	0	Mismatches 2	Indels 0	Gaps 0
OY	1	CTGAGACCGATATCG	15	
db	8	CTGAGACCGATATAG	22	

RESULT 28	
AZ304932/c	
LOCUS	43 bp DNA
DEFINITION	linear GSS 29-SEP-2000
ACCESSION	clone UUCG1M005G03 F, DNA sequence.
	AZ304932

VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 FEATURES
 SOURCE

AZ3045932.1 GI:10341444
 GSS.
 house mouse.
 Mus musculus
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 43)
 Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
 and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: dunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0005 row: G column: 03
 Seq primer: CGTTGTAAACGACGCGCCACT
 Class: plasmid ends
 High quality sequence stop: 43.
 Location/Qualifiers
 1..43

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BASE COUNT
ORIGIN
13 a          9 c          9 g          12 t

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="MGCIM0005G03"
/clone_lib="Mouse 10kb plasmid MGCIM library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD12 (g14732114[GB|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

	Query Match	86.6%;	Score 11.8;	DB 17;	Length 43;
	Best Local Similarity	53.7%;	Pred. No. 1.2e+05;		
	Matches 13; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;
OY	CGATATCGCTCTCAG	22			
db	22 CTATATGCTCTCAG	8			

RESULT 29			
LOCUS	AI003871		
DEFINITION	AI003871	48 bp	RNA linear EST 27-AUG-1998
	cc46cc6c.01	Soares testis	NHT Homo sapiens cDNA clone IMAGE:1619818
); similar to gb:M5531	GALACTOSIDE 2'-FLUCOSYLTRANSFERASE (HUMAN	
); contains MER14.b3	MER14 repetitive element); mRNA sequence.

ACCESSION AI003871
 VERSION AI003871.1 GI:3213381
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 48)
 NCICGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 Tumor Gene Index
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Unpublished (1997)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cgaps-r@mail.nih.gov
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bdrip/image/image.html

FEATURES
 source
 1..48
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:1619818"
 /clone_id="Soares_testis_NHT"
 /sex="male"
 /lab_host="DH10B"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTGGAGCGCGCCCAATTTTITTTTITTTT 3'].
 Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization to Cos5, and was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT
 10 a 4 c 8 g 26 t

ORIGIN

Query Match 52.7%; Score 11.6; DB 9; Length 48;
 Best Local Similarity 77.8%; Pred. No. 1.6e+05;
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 TGAGACGATTCGCTCT 19
 |||||
 29 TGAGACGATTCGCTCT 46
 |||||

RESULT 30
 AI003871/c 48 bp mRNA linear EST 27-AUG-1998
 LOCUS 0c46c06.e1 Soares_testis_NHT Homo sapiens CDNA clone IMAGE:1619818
 DEFINITION 3' similar to gp:M35531 GALACTOSIDE 2-L-FUCOSYLTRANSFERASE (HUMAN)
) contains MER14 repetitive element ;, mRNA sequence.
 ACCESSION AI003871
 VERSION AI003871.1 GI:3213381
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 48)
 NCICGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 Tumor Gene Index

JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-r@mail.nih.gov
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bdrip/image/image.html

FEATURES
 source
 1..48
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:1619818"
 /clone_id="Soares_testis_NHT"
 /sex="male"
 /lab_host="DH10B"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTGGAGCGCGCCCAATTTTITTTTITTTT 3'].
 Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization to Cos5, and was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT
 10 a 4 c 8 g 26 t

ORIGIN

Query Match 52.7%; Score 11.6; DB 9; Length 48;
 Best Local Similarity 77.8%; Pred. No. 1.6e+05;
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 AGACCGATTCGCTCTCA 21
 |||||
 46 AGACCGATTCGCTCTCA 29
 |||||

RESULT 31
 AI07186 50 bp mRNA linear EST 30-AUG-2001
 LOCUS AI07186 Sugano Homo sapiens CDNA library Homo sapiens CDNA clone
 DEFINITION K0709043, mRNA sequence.
 ACCESSION AI07186
 VERSION AI07186.1 GI:13556707
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 50)
 Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isegaki,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
 Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
 EMBO Rep. 2 (5), 388-393 (2001)
 JOURNAL Contact: Yutaka Suzuki
 MEDLINE Department of Medical Science, University of Tokyo
 21270072 Institute of Virology, Minatoku, Tokyo 108-8639, Japan
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: ysuzuki@ims.u-tokyo.ac.jp
 Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S.
 Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
source
Location/Qualifiers
1..50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="KAT09043"
/note="Differential display comparison of untreated and dimethylfluminate treated U937 cells"

BASE COUNT
11 a 11 c 13 g 15 t

Query Match 52.7%; Score 11.6; DB 9; Length 50;
Best Local Similarity 77.8%; Pred. No. 1.6e+05;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CTGAGACCGATTCGCTC 18
|||||
20 CTGAGACCAAGATGGCTC 37

RESULT 32
AU017186/c 50 bp mRNA linear EST 30-AUG-2001
LOCUS AU017186 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION KAT09043. mRNA sequence.
ACCESSION AU017186
VERSION AU017186.1 GI:13556707
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Suzuki, Y., Taira, H., Tsunoda, T., Mitsuhashi-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S.
Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
Location/Qualifiers
1..50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="KAT09043"
/note="Differential display comparison of untreated and dimethylfluminate treated U937 cells"

BASE COUNT
11 a 11 c 13 g 15 t

Query Match 52.7%; Score 11.6; DB 9; Length 50;
Best Local Similarity 77.8%; Pred. No. 1.6e+05;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 GACCGATTCGCTC 22
|||||
37 GACCGATTCGCTC 20

RESULT 33
AU013455 32 bp mRNA linear EST 03-AUG-1998
LOCUS AU013455 Schizosaccharomyces pombe late log phase cDNA
DEFINITION Schizosaccharomyces pombe cDNA clone spc08177, mRNA sequence.

ACCESSION AU013455.
AU013455.1 GI:3368246
KEYWORDS EST.
VERSION t15sion yeast.
SOURCE Schizosaccharomyces pombe
ORGANISM Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomycetes.
1 (bases 1 to 32)
Moriyomo, M. and Mita, K.
Identification of expressed sequence tags of Schizosaccharomyces pombe
Unpublished (1998)
Contact: Mitsunori Moriyomo
Genome Research Group
National Institute of Radiological Sciences
9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
Email: moriyomo@nirs.go.jp.
Location/Qualifiers
1..32
/organism="Schizosaccharomyces pombe"
/strain="972"
/db_xref="taxon:4896"
/clone="spc08177"
/sex="h minus"
/note="Vector: M13mp19. The cDNA library of Schizosaccharomyces pombe was prepared by cloning cDNA into the SmaI site of M13mp19 DNA and the direction of DNA sequences was not always from 5' to 3'. The cDNA data of Schizosaccharomyces pombe are available for searching on the World Wide Web. (URL: http://www.nirs.go.jp)"

BASE COUNT
12 a 5 c 11 g 3 t 1 others

Query Match 51.8%; Score 11.4; DB 9; Length 32;
Best Local Similarity 92.3%; Pred. No. 1.8e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GAGACCGATTCG 15
|||||
3 GAGACCGATTAAGC 15

RESULT 34
AU013455/c 32 bp mRNA linear EST 03-AUG-1998
LOCUS AU013455 Schizosaccharomyces pombe late log phase cDNA
DEFINITION Schizosaccharomyces pombe cDNA clone spc08177, mRNA sequence.
ACCESSION AU013455
VERSION AU013455.1 GI:3368246
KEYWORDS EST.
SOURCE t15sion yeast.
ORGANISM Schizosaccharomyces pombe
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomycetes.
1 (bases 1 to 32)
Moriyomo, M. and Mita, K.
Identification of expressed sequence tags of Schizosaccharomyces pombe
Unpublished (1998)
Contact: Mitsunori Moriyomo
Genome Research Group
National Institute of Radiological Sciences
9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
Email: moriyomo@nirs.go.jp.
Location/Qualifiers
1..32
/organism="Schizosaccharomyces pombe"
/strain="972"
/db_xref="taxon:4896"
/clone="spc08177"


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/clone.lib="Schizosaccharomyces pombe late log phase cDNA"
/sex="h minus"
/notes="Vector: M13mp19; The cDNA library of
Schizosaccharomyces pombe was prepared by cloning cDNA
into the SmaI site of M13mp19 DNA and the direction of DNA
sequences was not always from 5' to 3'. The cDNA data of
Schizosaccharomyces pombe are available for searching on
the World Wide Web. (URL, http://www.ntrs.go.jp)"
BASE COUNT      12 a      5 c      11 g      3 t      1 others
ORIGIN
Query Match      51.8%; Score 11.4; DB 9; Length 32;
Best Local Similarity 92.3%; Pred. NO. 1.8e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      8 CGATATCGCTCTC 20
      |||||
      |||||
      |||||
      |||||
      |||||
      15 CGCATATCGATCTC 3

RESULT 35
LOCUS      AU013784
DEFINITION AU013784 Schizosaccharomyces pombe cDNA clone spc08658, mRNA sequence.
ACCESSION AU013784
VERSION AU013784.1 GI:3368575
KEYWORDS EST.
SOURCE fission yeast.
ORGANISM Schizosaccharomyces pombe
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomycetes.
1 (bases 1 to 34)
Moriyama,M. and Mita,K.
Identification of expressed sequence tags of Schizosaccharomyces
pombe
Unpublished (1998)
Contact: Mitsunori Moriyama
Genome Research Group
National Institute of Radiological Sciences
9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
Email: moriyoma@nirs.go.jp.
Location/Qualifiers
1..34
/organism="Schizosaccharomyces pombe"
/strain="972"
/db_xref="taxon:4896"
/clone="spc08658"
/clone.lib="Schizosaccharomyces pombe late log phase cDNA"
/sex="h minus"
/notes="Vector: M13mp19; The cDNA library of
Schizosaccharomyces pombe was prepared by cloning cDNA
into the SmaI site of M13mp19 DNA and the direction of DNA
sequences was not always from 5' to 3'. The cDNA data of
Schizosaccharomyces pombe are available for searching on
the World Wide Web. (URL, http://www.ntrs.go.jp)"
BASE COUNT      12 a      6 c      12 g      4 t
ORIGIN
Query Match      51.8%; Score 11.4; DB 9; Length 34;
Best Local Similarity 92.3%; Pred. NO. 1.8e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      3 GAGACCGATATCG 15
      |||||
      |||||
      |||||
      |||||
      |||||
      Db      5 GAGACCGATATCG 17

RESULT 36
LOCUS      AU013784
DEFINITION AU013784 Schizosaccharomyces pombe late log phase cDNA

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ACCESSION	Schizosaccharomyces pombe cDNA clone spc08658, mRNA sequence.
VERSION	AU013784
KEYWORDS	AU013784.1 GI:3368575 EST. <i>fission yeast</i> .
SOURCE	Schizosaccharomyces pombe
ORGANISM	Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomyces. 1 (bases 1 to 34) Moriyomo,M. and Mita,K. Identification of expressed sequence tags of Schizosaccharomyces pombe
JOURNAL COMMENT	Unpublished (1998) Contact: Mitsunuki Moriyomo Genome Research Group National Institute of Radiological Sciences 9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan Email: moriyomo@nirs.go.jp Location/Qualifiers 1..34 /organism="Schizosaccharomyces pombe" /strain="972" /db_xref="taxon:4896" /cclone="spc08658" /sex="h minus" /note="Vector: M13mp19; The cDNA library of Schizosaccharomyces pombe was prepared by cloning cDNAs into the SmaI site of M13mp19 DNA and the direction of DNA sequences was not always from 5' to 3'. The cDNA data of Schizosaccharomyces pombe are available for searching on the World Wide Web. (URL, http://www.nirs.go.jp)" BASE COUNT 12 a 6 c 12 g 4 t ORIGIN
FEATURES	Source
CY	8 CGATATCGGTCTC 20 Db 17 GCCTAAGGTTCTC 5
RESULT 37	
LOCUS	AU013851 34 bp mRNA linear EST 03-AUG-1998
DEFINITION	AU013851 Schizosaccharomyces pombe late log phase cDNA
ACCESSION	Schizosaccharomyces pombe cDNA clone spc08749, mRNA sequence.
VERSION	AU013851
KEYWORDS	AU013851.1 GI:3368642 EST. <i>fission yeast</i> . Schizosaccharomyces pombe Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomyces. 1 (bases 1 to 34) Moriyomo,M. and Mita,K. Identification of expressed sequence tags of Schizosaccharomyces pombe
JOURNAL COMMENT	Unpublished (1998) Contact: Mitsunuki Moriyomo Genome Research Group National Institute of Radiological Sciences 9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan Email: moriyomo@nirs.go.jp Location/Qualifiers 1..34 /organism="Schizosaccharomyces pombe" /strain="972" /db_xref="taxon:4896"

/clone="spc08749"
/clone.lib="Schizosaccharomyces pombe late log phase cDNA"
/sex="f minus"
/note="Vector: M13mp19, The cDNA library of Schizosaccharomyces pombe was prepared by cloning cDNA into the SmaI site of M13mp19 DNA and the direction of DNA sequences was not always from 5' to 3'. The cDNA data of Schizosaccharomyces pombe are available for searching on the World Wide Web. (URL, <http://www.nirs.go.jp>)"

BASE COUNT 12 a 6 c 12 g 4 t

ORIGIN

Query Match 51.8%; Score 11.4; DB 9; Length 34;
Best Local Similarity 92.3%; Pred. No. 1.8e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GAGACCGATATCG 15
|||||
5 GAGACCGATACCG 17

Db

RESULT 38
AU013851/c 34 bp mRNA linear EST 03-AUG-1998
LOCUS
DEFINITION AU013851 Schizosaccharomyces pombe late log phase cDNA
ACCESSION AU013851
VERSION AU013851.1 GI:3368642
KEYWORDS EST.
SOURCE fission yeast.
ORGANISM Schizosaccharomyces pombe
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
1 (bases 1 to 34)
Moriyomo, M. and Mita, K.
TITLE Identification of expressed sequence tags of Schizosaccharomyces pombe
JOURNAL Unpublished (1998)
COMMENT Contact: Mitsuoki Moriyomo
Genome Research Group
National Institute of Radiological Sciences
9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
Email: moriyomo@nirs.go.jp.
FEATURES
SOURCE location/Qualifiers
1..34
/organism="Schizosaccharomyces pombe"
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/db_xref="taxon:4896"
/clone="spc08749"
/clone.lib="Schizosaccharomyces pombe late log phase cDNA"
/sex="f minus"
/note="Vector: M13mp19, The cDNA library of Schizosaccharomyces pombe was prepared by cloning cDNA into the SmaI site of M13mp19 DNA and the direction of DNA sequences was not always from 5' to 3'. The cDNA data of Schizosaccharomyces pombe are available for searching on the World Wide Web. (URL, <http://www.nirs.go.jp>)"

BASE COUNT 12 a 6 c 12 g 4 t

ORIGIN

Query Match 51.8%; Score 11.4; DB 9; Length 34;
Best Local Similarity 92.3%; Pred. No. 1.8e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CGATATCGGTCTC 20
|||||
17 CGGTATCGGTCTC 5

Db

RESULT 39
AV833036 38 bp mRNA linear EST 22-JUN-2001
LOCUS

DEFINITION AV833036 K. Sato unpublished cDNA library: Hordeum vulgare subsp. vulgare shoots germination Hordeum vulgare subsp. vulgare cDNA clone bags10c17, mRNA sequence.
AV833036
VERSION AV833036.1 GI:14525125
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. vulgare.
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae / Triticeae; Hordeum.
1 (bases 1 to 38)
Sato, K.
REFERENCE Barley EST sequencing project in NIG and Okayama Univ Unpublished (2001)
AUTHORS Contact: Kazuhiro Sato
TITLE Research Institute for Bioresources
JOURNAL Okayama University, Barley Germplasm Center
COMMENT Chuo 2-20-1, Kurashiki, Okayama 710-0046, Japan
Email: kazsato@rib.okayama-u.ac.jp,
URL: <http://www.rib.okayama-u.ac.jp/barley/>
Sato, K., Saitoh, D., Takeda, K., Shini, T. and Kohara, Y. Direct submission:
database: <http://www.shigen.nig.ac.jp/barley/Barley.html>.

FEATURES
SOURCE location/Qualifiers
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/organism="Hordeum vulgare subsp. vulgare"
/cultivar="Haruna Nijo"
/db_xref="taxon:112509"
/clone="bags10c17"
/clone.lib="K. Sato unpublished cDNA library: Hordeum vulgare subsp. vulgare shoots germination"
/tissue type="shoots"
/dev_stage="germination"

BASE COUNT 11 a 8 c 8 g 11 t

ORIGIN

Query Match 51.8%; Score 11.4; DB 10; Length 38;
Best Local Similarity 92.3%; Pred. No. 1.8e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 GATATCGGTCTCA 21
|||||
13 GATATCGGTCTCA 25

Db

RESULT 40
AV833036 38 bp mRNA linear EST 22-JUN-2001
LOCUS AV833036 K. Sato unpublished cDNA library: Hordeum vulgare subsp. vulgare shoots germination Hordeum vulgare subsp. vulgare cDNA clone bags10c17, mRNA sequence.
DEFINITION AV833036 K. Sato unpublished cDNA library: Hordeum vulgare subsp. vulgare cDNA clone bags10c17, mRNA sequence.
AV833036
VERSION AV833036.1 GI:14525125
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. vulgare.
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae / Triticeae; Hordeum.
1 (bases 1 to 38)
Sato, K.
REFERENCE Barley EST sequencing project in NIG and Okayama Univ Unpublished (2001)
AUTHORS Contact: Kazuhiro Sato
TITLE Research Institute for Bioresources
JOURNAL Okayama University, Barley Germplasm Center
COMMENT Chuo 2-20-1, Kurashiki, Okayama 710-0046, Japan
Email: kazsato@rib.okayama-u.ac.jp,
URL: <http://www.rib.okayama-u.ac.jp/barley/>
Sato, K., Saitoh, D., Takeda, K., Shini, T. and Kohara, Y. Direct submission:
database: <http://www.shigen.nig.ac.jp/barley/Barley.html>.

FEATURES
source

Location/Qualifiers
1. .38
/organism="Hordeum vulgare subsp. vulgare"
/cultivar="Haruna Nijo"
/db_xref="taxon:112509"
/clone="bags10c17"
/clone_id="K. Sato unpublished cDNA library: Hordeum
vulgare subsp. vulgare shoots germination"
/issue_type="shoots"
/dev_stage="germination"
BASE COUNT 11 a 8 c 8 g 11 t
ORIGIN

Query Match 51.8%; Score 11.4; DB 10; Length 38;
Best Local Similarity 92.3%; Pred. No. 1.8e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGAGACCGATATC 14
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Db 25 TGAGACCGATATC 13

Search completed: June 14, 2003, 22:37:59
Job time : 1390 secs

